TITLE OF THE INVENTION

GlcNAc PHOSPHOTRANSFERASE OF THE LYSOSOMAL TARGETING PATHWAY

BACKGROUND OF THE INVENTION

Field of the Invention

This invention relates generally to enzymes involved in the lysosomal targeting pathway and particularly to isolated and purified GlcNAc-phosphotransferase and phosphodiester α-GlcNAcase, nucleic acids encoding the enzymes, processes for production of recombinant GlcNAc-phosphotransferase and phosphodiester α-GlcNAcase, and the use of the enzymes for the preparation of highly phosphorylated lysosomal enzymes that are useful for the treatment of lysosomal storage diseases.

Description of the Prior Art

Lysosomes and Lysosomal Storage Diseases

Lysosomes are organelles in eukaryotic cells that function in the degradation of macromolecules into component parts that can be reused in biosynthetic pathways or discharged by the cell as waste. Normally, these macromolecules are broken down by enzymes known as lysosomal enzymes or lysosomal hydrolases. However, when a lysosomal enzyme is not present in the lysosome or does not function properly, the enzymes specific macromolecular substrate accumulates in the lysosome as "storage material" causing a variety of diseases, collectively known as lysosomal storage diseases.

Lysosomal storage diseases can cause chronic illness and death in hundreds of

individuals each year. There are approximately 50 known lysosomal storage diseases, e.g., Pompe Disease, Hurler Syndrome, Fabry Disease, Maroteaux-Lamy Syndrome (mucopolysaccharidosis VI), Morquio Syndrome (mucopolysaccharidosis IV), Hunter Syndrome (mucopolysaccharidosis II), Farber Disease, Acid Lipase Deficiency, Krabbe Disease, and Sly Syndrome (mucopolysaccharidosis VII). In each of these diseases, lysosomes are unable to degrade a specific compound or group of compounds because the enzyme that catalyzes a specific degradation reaction is missing from the lysosome, is present in low concentrations in the lysosome, or is present at sufficient concentrations in the lysosome but is not functioning properly.

Lysosomal storage diseases have been studied extensively and the enzymes (or lack thereof) responsible for particular diseases have been identified. Most of the diseases are caused by a deficiency of the appropriate enzyme in the lysosome, often due to mutations or deletions in the structural gene for the enzyme. For some lysosomal storage diseases, the enzyme deficiency is caused by the inability of the cell to target and transport the enzymes to the lysosome, e.g., I-cell disease and pseudo-Hurler polydystrophy.

Lysosomal Storage diseases have been studied extensively and the enzymes (or lack thereof) responsible for particular diseases have been identified (Scriver, Beaudet, Sly, and Vale, eds., The Metabolic Basis of Inherited Disease, 6th Edition, 1989, Lysosomal Enzymes, Part 11, Chapters 61-72, pp. 1565-1839). Within each disease, the severity and the age at which the disease presents may be a function of the amount of residual lysosomal enzyme that exists in the patient.

Lysosomal Targeting Pathway

The lysosomal targeting pathways have been studied extensively and the process by

which lysosomal enzymes are synthesized and transported to the lysosome has been well described. Kornfeld, S. (1986). "Trafficking of lysosomal enzymes in normal and disease states." *Journal of Clinical Investigation* 77: 1-6 and Kornfeld, S. (1990). "Lysosomal enzyme targeting." *Biochem. Soc. Trans.* 18: 367-374. Generally, lysosomal enzymes are synthesized by membrane-bound polysomes in the rough endoplastic reticulum ("RER") along with secretory glycoproteins. In the RER, lysosomal enzymes acquire N-linked oligosaccharides by the en-bloc transfer of a preformed oligosaccharide from dolichol phosphate containing 2 N-acetylglucosamine, 9-mannose and 3-glucose. Glycosylated lysosomal enzymes are then transported to the Golgi apparatus along with secretory proteins. In the cis-Golgi or intermediate compartment lysosomal enzymes are specifically and uniquely modified by the transfer of GlcNAc-phosphate to specific mannoses. In a second step, the GlcNAc is removed thereby exposing the mannose 6-phosphate ("M6P") targeting determinant. The lysosomal enzymes with the exposed M6P binds to M6P receptors in the trans-Golgi and is transported to the endosome and then to the lysosome. In the lysosome, the phosphates are rapidly removed by lysosomal phosphatases and the mannoses are removed by lysosomal mannosidases (Einstein, R. and Gabel, C.A. (1991). "Cell- and ligand-specific deposphorylation of acid hydrolases: evidence that the mannose 6-phosphate is controlled by compartmentalization." *Journal of Cell Biology* 112: 81-94).

The synthesis of lysosomal enzymes having exposed M6P is catalyzed by two different enzymes, both of which are essential if the synthesis is to occur. The first enzyme is UDP-N-acetylglucosamine: lysosomal enzyme N-Acetylglucosamine-1-phosphotransferase ("GlcNAc-phosphotransferase") (E.C. 2.7.8.17). GlcNAc-phosphotransferase catalyzes the transfer of N-acetylglucosamine-1-phosphate from UDP-GlcNAc to the 6 position of α1,2-linked mannoses on the lysosomal enzyme. The

recognition and addition of N-acetylgluocosamine-1-phosphate to lysosomal hydrolases by GlcNAc-phosphotransferase is the critical and determining step in lysosomal targeting. The second step is catalyzed by N-acetylglucosamine-1-phosphodiester α-N-Acetylglucosaminidase ("phosphodiester α-GlcNAcase") (E.C. 3.1.4.45). Phosphodiester α-GlcNAcase catalyzes the removal of N-Acetylglucosamine from the GlcNAc-phosphate modified lysosomal enzyme to generate a terminal M6P on the lysosomal enzyme. Preliminary studies of these enzymes have been conducted. Bao *et al.*, in *The Journal of Biological Chemistry,* Vol. 271, Number 49, Issue of December 6, 1996, pp. 31437-31445, relates to a method for the purification of bovine UDP-N-acetylglucosamine: Lysosomal enzyme N-Acetylglucosamine-l-phosphotransferase and proposes a hypothetical subunit structure for the protein. Bao *et al.*, in *The Journal of Biological Chemistry,* Vol. 271, Number 49, Issue of December 6, 1996, pp. 31446-31451, relates to the enzymatic characterization and identification of the catalytic subunit for bovine UDP-N-acetylglucosamine: Lysosomal enzyme N-Acetylglucosamine-1-phosphotransferase. Kornfeld *et al.*, in *The Journal of Biological Chemistry,* Vol. 273, Number 36, Issue of September 4, 1998, pp. 23203-23210, relates to the purification and multimeric structure of bovine N-Acetylglucosamine-l-phosphodiester α-N-Acetylglucosaminidase. However, the proprietary monoclonal antibodies required to isolate these proteins have not been made available to others and the protein sequences for the enzymes used in these preliminary studies have not been disclosed.

Although the lysosomal targeting pathway is known and the naturally occurring enzymes involved in the pathway have been partially studied, the enzymes responsible for adding M6P in the lysosomal targeting pathway are difficult to isolate and purify and are poorly understood. A better understanding of the lysosomal targeting pathway enzymes and

the molecular basis for their action is needed to assist with the development of effective techniques for the utilization of these enzymes in methods for the treatment of lysosomal storage diseases, particularly in the area of targeted enzyme replacement therapy.

Treatment of Lysosomal Storage Diseases

Lysosomal storage diseases caused by the lack of enzymes can in theory be treated using enzyme replacement therapy, *i.e.,* by administering isolated and purified enzymes to the patient to treat the disease. However, to be effective, the lysosomal enzyme administered must be internalized by the cell and transported to the lysosome. Naturally occurring enzymes and their recombinant equivalents, however, have been of limited value in enzyme replacement therapy because the purified or recombinant lysosomal enzymes do not contain adequate amounts of exposed M6P, or contain undesirable oligosaccharides which mediates their destruction. Without sufficient M6P, the administered lysosomal enzyme cannot efficiently bind to M6P receptors and be transported to the lysosome. For example, human acid α-glucosidase purified from placenta contains oligomannose oligosaccharides which are not phosphorylated (Mutsaers, J. H. G. M., Van Halbeek, H., Vliegenthart, J. F. G., Tager, J. M., Reuser, A. J. J., Kroos, M., and Galjaard, H. (1987). "Determination of the structure of the carbohydrate chains of acid α-glucosidase from human placenta." *Biochimica et Biophysica Acta* 911: 244 - 251), and this glycoform of the enzyme is not efficiently internalized by cells (Reuser, A. J., Kroos, M. A., Ponne, N. J., Wolterman, R. A., Loonen, M. C., Busch, H. F., Visser, W. J., and Bolhuis, P. A. (1984). "Uptake and stability of human and bovine acid alpha-glucosidase in cultured fibroblasts and skeletal muscle cells from glycogenosis type II patients." *Experimental Cell Research* 155: 178-189). As a result

of the inability to purify or synthesize lysosomal enzymes with the desired oligosaccharide structures, these enzyme preparations are inefficiently targeted to affected cells and are of limited effectiveness in the treatment of these diseases. There exists, therefore, a need for enzymes that can be used in enzyme replacement therapy procedures, particularly highly phosphorylated enzymes that will be efficiently internalized by the cell and transported to the lysosome.

SUMMARY OF THE INVENTION

It is, therefore, an object of the present invention to provide biologically active GlcNAc-phosphotransferase and phosphodiester α-GlcNAcase as isolated and purified polypeptides.

It is another object of the present invention to provide nucleic acid molecules encoding GlcNAc-phosphotransferase and phosphodiester α-GlcNAcase.

It is another object of the present invention to provide expression vectors having DNA that encodes GlcNAc-phosphotransferase and phosphodiester α-GlcNAcase.

It is a further object of the present invention to provide host cells that have been transfected with expression vectors having DNA that encodes GlcNAc-phosphotransferase or phosphodiester α-GlcNAcase.

It is another object of the present invention to provide methods for producing recombinant GlcNAc-phosphotransferase and recombinant phosphodiester α-GlcNAcase by culturing host cells that have been transfected or transformed with expression vectors having DNA that encodes GlcNAc-phosphotransferase or phosphodiester α-GlcNAcase.

It is another object of the present invention to provide isolated and purified

recombinant GlcNAc-phosphotransferase and recombinant phosphodiester α-GlcNAcase.

It is another object of the present invention to provide methods for the preparation of highly phosphorlyated lysosomal enzymes that are useful for the treatment of lysosomal storage diseases.

It is a further object of the present invention to provide highly phosphorlyated lysosomal hydrolases that are useful for the treatment of lysosomal storage diseases.

It is still another object of the present invention to provide methods for the treatment of lysosomal storage diseases.

It is still another object of the present invention to provide monoclonal antibodies capable of selectively binding to bovine GlcNAc-phosphotransferase and to bovine phosphodiester α-GlcNAcase.

These and other objects are achieved by recovering isolated and purified biologically active GlcNAc-phosphotransferase and phosphodiester α-GlcNAcase and using the enzymes to obtain nucleic acid molecules that encode for the enzymes. The nucleic acid molecules coding for either enzyme are incorporated into expression vectors that are used to transfect host cells that express the enzyme. The expressed enzyme is recovered and used to prepare highly phosphorylated lysosomal hydrolases useful for the treatment of lysosomal storage diseases. In particular, the enzymes are used to produce highly phosphorylated-lysosomal hydrolases that can be effectively used in enzyme replacement therapy procedures.

Lysosomal hydrolases having high mannose structures are treated with GlcNAc-phosphotransferase and phosphodiester α-GlcNAcase resulting in the production of asparagine-linked oligosaccharides that are highly modified with mannose 6-phosphate ("M6P"). The treated hydrolase binds to M6P receptors on the cell membrane and is transported into the cell and delivered to the lysosome where it can perform its normal or a

desired function.

Other aspects and advantages of the present invention will become apparent from the following more detailed description of the invention taken in conjunction with the accompanying drawings.

BRIEF OF DESCRIPTION OF THE DRAWINGS

Figure 1 shows a model of the subunit structure of GlcNAc-phosphotransferase. The enzyme is a complex of six polypeptides. The α- and β-subunits are the product of a single gene. Following translation, the α- and β-subunits are separated by proteolytic cleavage between Lys^{929} and Asp^{930}. The α-subunit is a type II membrane glycoprotein with a single amino terminal membrane spanning domain. The β-subunit is a type I membrane spanning glycoprotein with a single carboxyl terminal membrane spanning domain. The γ-subunit is the product of a second gene. The γ-subunit is a soluble protein with a cleaved signal peptide. The α-, β-, and γ-subunits are all tightly associated.

Figure 2 shows a model of the subunit structure of phosphodiester α-GlcNAcase. The enzyme is a tetramer composed of four identical subunits arranged as two non-covalently-associated dimers which are themselves disulfide-linked. The single subunit is a type I membrane protein containing a signal peptide, a pro region not present in the mature enzyme and a single carboxyl terminal membrane spanning domain.

Figure 3 shows a diagram of recombinant glycoprotein expression in CHO cells. In overexpressing CHO cells, the rh-GAA is processed along the pathways 1 and 2, depending on whether or not the enzyme is acted upon by GlcNAc-phosphotransferase (GnPT). Secreted GAA contains predominantly sialylated biantenniary complex-type glycans and is not a substrate for GlcNAc-phosphotransferase. In the presence of the α1,2-mannosidase

inhibitors, 1-deoxymannojirimycin or kifunensine conversion of MAN9 to MAN5 structures is blocked, resulting in secretion of GAA-bearing MAN7-9 structures which can be modified with GlcNAc-phosphotransferase and phosphodiester α-GlcNAcase (UCE) generating phosphorylated species (pathway 3).

Figure 4 shows transient expression analysis of various plasmid constucts of the α/β and γ subunits of human GlcNAc-phosphotransferase. Plasmids containing the α/β and/or the γ subunits were transfected into 293T cells, the expressed protein was purified from the culture at 23, 44.5 and 70 hours after transfection and relative amounts of expression were assessed by measuring phosphotransferase activity using methyl-α-D-mannoside and [β-^{32}P] UDP-GlcNAc as substrates.

DETAILED DESCRIPTION OF THE INVENTION

The term "GlcNAc-phosphotransferase" as used herein refers to enzymes that are capable of catalyzing the transfer of N-acetylglucosamine-l-phosphate from UDP-GlcNAc to the 6' position of αl,2-linked mannoses on lysosomal enzymes.

The term "phosphodiester α-GlcNAcase" as used herein refers to enzymes that are capable of catalyzing the removal of N-Acetylglucosamine from GlcNAc-phosphate-mannose diester modified lysosomal enzymes to generate terminal M6P.

The terms "GlcNAc-phosphotransferase" and "phosphodiester α-GlcNAcase" as used herein refer to enzymes obtained from any eukaryotic species, particularly mammalian species such as bovine, porcine, murine, equine, and human, and from any source whether natural, synthetic, semi-synthetic, or recombinant. The terms encompass membrane-bound enzymes and soluble or truncated enzymes having less than the complete amino acid

sequence and biologically active variants and gene products.

The term "naturally occurring" as used herein means an endogenous or exogenous protein isolated and purified from animal tissue or cells.

The term "isolated and purified" as used herein means a protein that is essentially free of association with other proteins or polypeptides, *e.g.*, as a naturally occurring protein that has been separated from cellular and other contaminants by the use of antibodies or other methods or as a purification product of a recombinant host cell culture.

The term "biologically active" as used herein means an enzyme or protein having structural, regulatory, or biochemical functions of a naturally occurring molecule.

The term "nucleotide sequence" as used herein means a polynucleotide molecule in the form of a separate fragment or as a component of a larger nucleic acid construct that has been derived from DNA or RNA isolated at least once in substantially pure form *(i.e.,* free of contaminating endogenous materials) and in a quantity or concentration enabling identification, manipulation, and recovery of its component nucleotide sequences by standard biochemical methods. Such sequences are preferably provided in the form of an open reading frame uninterrupted by internal non-translated sequences, or introns that are typically present in eukaryotic genes. Sequences of non-translated DNA may be present 5' or 3' from an open reading frame where the same do not interfere with manipulation or expression of the coding region.

The term "nucleic acid molecule" as used herein means RNA or DNA, including cDNA, single or double stranded, and linear or covalently closed molecules. A nucleic acid molecule may also be genomic DNA corresponding to the entire gene or a substantial portion therefor to fragments and derivatives thereof. The nucleotide sequence may correspond to the naturally occurring nucleotide sequence or may contain single or multiple nucleotide

substitutions, deletions and/or additions including fragments thereof. All such variations in the nucleic acid molecule retain the ability to encode a biologically active enzyme when expressed in the appropriate host or an enzymatically active fragment thereof. The nucleic acid molecule of the present invention may comprise solely the nucleotide sequence encoding an enzyme or may be part of a larger nucleic acid molecule that extends to the gene for the enzyme. The non-enzyme encoding sequences in a larger nucleic acid molecule may include vector, promoter, terminator, enhancer, replication, signal sequences, or non-coding regions of the gene.

The term "variant" as used herein means a polypeptide substantially homologous to a naturally occurring protein but which has an amino acid sequence different from the naturally occurring protein (human, bovine, ovine, porcine, murine, equine, or other eukaryotic species) because of one or more deletions, insertions, derivations, or substitutions. The variant amino acid sequence preferably is at least 50% identical to a naturally occurring amino acid sequence but is most preferably at least 70% identical. Variants may comprise conservatively substituted sequences wherein a given amino acid residue is replaced by a residue having similar physiochemical characteristics. Conservative substitutions are well known in the art and include substitution of one aliphatic residue for another, such as Ile, Val, Leu, or Ala for one another, or substitutions of one polar residue for another, such as between Lys and Arg; Glu and Asp; or Gln and Asn. Conventional procedures and methods can be used for making and using such variants. Other such conservative substitutions such as substitutions of entire regions having similar hydrophobicity characteristics are well known. Naturally occurring variants are also encompassed by the present invention. Examples of such variants are enzymes that result from alternate mRNA splicing events or from proteolytic cleavage of the enzyme that leave the enzyme biologically active and

capable of performing its catalytic function. Alternate splicing of mRNA may yield a truncated but biologically active protein such as a naturally occurring soluble form of the protein. Variations attributable to proteolysis include differences in the N- or C-termini upon expression in different types of host cells due to proteolytic removal of one or more terminal amino acids from the protein.

The term "substantially the same" as used herein means nucleic acid or amino acid sequences having sequence variations that do not materially affect the nature of the protein, i.e., the structure and/or biological activity of the protein. With particular reference to nucleic acid sequences, the term"substantially the same" is intended to refer to the coding region and to conserved sequences governing expression and refers primarily to degenerate codons encoding the same amino acid or alternate codons encoding conservative substitute amino acids in the encoded polypeptide. With reference to amino acid sequences, the term "substantially the same" refers generally to conservative substitutions and/or variations in regions of the polypeptide nor involved in determination of structure or function.

The term "percent identity" as used herein means comparisons among amino acid sequences as defined in the UWGCG sequence analysis program available from the University of Wisconsin. (Devereaux *et al.*, Nucl. Acids Res. 12: 387-397 (1984)).

The term "highly phosphorylated lysosomal hydrolase" as used to herein means a level of phosphorylation on a purified lysosomal hydrolase which could not be obtained by only isolating the hydrolase from a natural source and without subsequent treatment with the GlcNAc-phosphotransferase and phosphodiester-α-GlcNAcase. In particular, "highly phosphorylated lysosomal hydrolase" means a lysosomal hydrolase that contains from about 6% to about 100% bis-phosphorylated oligosaccharides.

This invention is not limited to the particular methodology, protocols, cell lines,

vectors, and reagents described because these may vary. Further, the terminology used herein is for the purpose of describing particular embodiments only and is not intended to limit the scope of the present invention. As used herein and in the appended claims, the singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise, *e.g.,* reference to "a host cell") includes a plurality of such host cells.

Because of the degeneracy of the genetic code, a multitude of nucleotide sequences encoding GlcNAc-phosphotransferase, phosphodiester α-GlcNAcase, or other sequences referred to herein may be produced. Some of these sequences will be highly homologous and some will be minimally homologous to the nucleotide sequences of any known and naturally occurring gene. The present invention contemplates each and every possible variation of nucleotide sequence that could be made by selecting combinations based on possible codon choices. These combinations are made in accordance with the standard triplet genetic code as applied to the nucleotide sequence of naturally occurring GlcNAc-phosphotransferase or phosphodiester α-GlcNAcase, and all such variations are to be considered as being specifically disclosed.

Unless defined otherwise, all technical and scientific terms and any acronyms used herein have the same meanings as commonly understood by one of ordinary skill in the art in the field of the invention. Although any methods and materials similar or equivalent to those described herein can be used in the practice of the present invention, the preferred methods, devices, and materials are described herein.

All patents and publications mentioned herein are incorporated herein by reference to the extent allowed by law for the purpose of describing and disclosing the proteins, enzymes, vectors, host cells, and methodologies reported therein that might be used with the present invention. However, nothing herein is to be construed as an admission that the invention is

not entitled to antedate such disclosure by virtue of prior invention.

The Invention

GlcNAc-phosphotransferase

In one aspect, the present invention provides isolated and purified biologically active GlcNAc-phosphotransferase, nucleic acid molecules encoding GlcNAc-phosphotransferase and its subunits, expression vectors having a DNA that encodes GlcNAc-phosphotransferase, host cells that have been transfected or transformed with expression vectors having DNA that encodes GlcNAc-phosphotransferase, methods for producing recombinant GlcNAc-phosphotransferase by culturing host cells that have been transfected or transformed with expression vectors having DNA that encodes GlcNAc-phosphotransferase, isolated and purified recombinant GlcNAc-phosphotransferase, and methods for using GlcNAc-phosphotransferase for the preparation of highly phosphorylated lysosomal enzymes that are useful for the treatment of lysosomal storage diseases.

To obtain isolated and purified GlcNAc-phosphotransferase and its subunits and the nucleic acid molecules encoding the enzyme according to the present invention, bovine GlcNAc phosphotransferase was obtained and analyzed as follows. Splenocytes from mice immunized with a partially purified preparation of bovine GlcNAc-phosphotransferase were fused with myeloma cells to generate a panel of hybridomas. Hybridomas secreting monoclonal antibodies specific for GlcNAc-phosphotransferase were identified by immunocapture assay. In this assay, antibodies which could capture GlcNAc-phosphotransferase from a crude source were identified by assay of immunoprecipitates with a specific GlcNAc-phosphotransferase enzymatic assay. Hybridomas were subcloned twice, antibody produced in ascites culture, coupled to a solid support and evaluated for

immunoaffinity chromatography. Monoclonal PT18-Emphaze was found to allow a single step purification of GlcNAc-phosphotransferase to homogeneity. Bao, *et.al.*, The Journal of Biological Chemistry, Vol. 271, Number 49, Issue of December 6, 1996, pp. 31437-31445 relates to a method for the purification of bovine UDP-N-acetylglucosamine:Lysosomal-enzyme N-Acetylglucosamine-l-phosphotransferase and proposes a hypothetical subunit structure for the protein. Bao, *et. al., The Journal of Biological Chemistry,* Vol. 271, Number 49, Issue of December 6, 1996, pp. 31446-31451. Using this technique, the enzyme was purified 488,000-fold in 29% yield. The eluted GlcNAc-phosphotransferase has a specific activity of $>10^6$, preferably $>5x10^6$, more preferably $>12x10^6$ pmol/h/mg and is apparently a homogenous, multi-subunit enzyme based on silver-stained SDS-PAGE. The monoclonal antibody labeled PT18 was selected for use in further experiments. A hybridoma secreting monoclonal antibody PT 18 was deposited with the American Type Culture Collection, 10801 Univerisity Blvd., Manassas, VA 20110 and assigned ATCC Accession No. _____.

GlcNAc-phosphotransferase was determined to be a complex of six polypeptides with a subunit structure $\alpha_2\beta_2\gamma_2$. Figure 1 shows a model of the subunit structure obtained from quantitative amino acid sequencing, immunoprecipitation with subunit-specific monoclonal antibodies, SDS-PAGE, and cDNA sequences. The evidence for the model is summarized below. The molecular mass of the complex estimated by gel filtration is 570,000 Daltons. The 166,000 Dalton α-subunit is found as a disulfide-linked homodimer. Likewise, the 51,000 Dalton γ-subunit is found as a disulfide-linked homodimer. Because both the α- and γ-subunits are found in disulfide-linked homodimers, each molecule must contain at least one α- and one γ homodimer. Although the 56,000 Dalton β-subunit is not found in a disulfide-linked homodimer, two independent lines of evidence strongly suggest each

complex contains two β-subunits as well. First, quantitative aminoterminal sequencing demonstrates a 1:1 molar ratio between the β- and γ-subunits. Secondly, since the α- and β-subunits are encoded by a single cDNA and divided by proteolytic processing, two β-subunits are produced for each α-subunit dimer. The predicted mass of the complex based on the composition $\alpha_2\beta_2\gamma_2$ is 546,000 Daltons (2 x 166,000 + 2 x 56,000 + 2x 51,000) in excellent agreement with the mass estimated by gel filtration.

GlcNAc-phosphotransferase was purified using an assay for the transfer of GlcNAc-l-Phosphate to the synthetic acceptor α-methylmannoside. However, the natural acceptors for GlcNAc-phosphotransferase are the high mannose oligosaccharides of lysosomal hydrolases. To evaluate the ability of the purified GlcNAc-phosphotransferase to utilize glycoproteins as acceptors, the transfer of GlcNAc-l-P to the lysosomal enzymes uteroferrin and cathepsin D, the nonlysosomal glycoprotein RNAse B, and the lysosomal hydrolase β-glucocerebrosidase (which is trafficked by a M6P independent pathway), were investigated. Both uteroferrin and cathepsin D are effectively utilized as acceptors by purified GlcNAc-phosphotransferase with K_ms below 20 μm. In contrast, neither RNAse B nor β-glucocerebrosidase is an effective acceptor.

The ineffectiveness of RNAse B, which contains a single high mannose oligosaccharide, as an acceptor is especially notable since the K_m was not reached at the solubility limit of the protein (at 600 μm). This data clearly demonstrates the specific phosphorylation of Lysosomal hydrolases previously observed with crude preparations (Waheed, Pohlmann A., R., *et al.* (1982). "Deficiency of UDP-N-acetylglucosamine:lysosomal enzyme N-Acetylglucosamine-lphosphotransferase in organs of I-Cell patients." *Biochemical and Biophysical Research Communications* 105(3): 1052-10580 is a property of the GlcNAc-phosphotransferase itself.

The α-subunit was identified as containing the UDP-GlcNAc binding site since this subunit was specifically photoaffinity-labeled with [β-^{32}P]-5-azido-UDP-Glc.

The amino-terminal and internal (tryptic) protein sequence data was obtained for each subunit. N-terminal sequence was obtained from each subunit as follows. Individual subunits of GlcNAc-phosphotransferase were resolved by polyacrylamide gel electrophoresis in the presence of sodium dodecyl sulfate before and after disulfide bond reduction. Subunits were then transferred to a PVDF membrane by electroblotting, identified by Coomassie blue staining, excised, and subjected to N-terminal sequencing. To obtain internal sequence, GlcNAc-phosphotransferase was denatured, reduced, and alkylated, and individual subunits were resolved by gel filtration chromatography. Isolated subunits were then digested with trypsin and the tryptic peptides fractionated by reverse phase HPLC. Peaks which appeared to contain only a single peptide were analyzed for purity by MALDI and subjected to N-terminal amino acid sequencing.

The amino acid sequence for the human α-subunit is shown in amino acids 1-928 of SEQ ID NO: 1; the human β-subunit in amino acids 1-328 of SEQ ID NO:2; and the human γ-subunit in amino acids 25-305 of SEQ ID NO:3. The γ-subunit has a signal sequence shown in amino acids 1-24 of SEQ ID NO:3.

Comparison with the databases using the blast algorithms demonstrate these proteins have not been previously described although several EST sequences of the corresponding cDNAs are present.

Using these peptide sequences and a combination of library screening, RACE, PCR and Blast searching of expressed sequence tag ("EST") files, full-length human cDNAs encoding each subunit were cloned and sequenced.

The nucleotide sequence for the human α/β-subunit precursor cDNA is shown in

nucleotides 165-3932 of SEQ ID NO:4; the nucleotide sequence for the α-subunit is shown in nucleotides 165-2948 of SEQ ID NO:4; the nucleotide sequence for the β-subunit is shown in nucleotides 2949-3932 of SEQ ID NO:4; and the nucleotide sequence for the γ-subunit is shown in nucleotides 96-941 of SEQ ID NO:5. The nucleotide sequence for the γ-subunit signal peptide is shown in nucleotides 24-95 of SEQ ID NO:5.

For each subunit a N-terminal peptide and two internal peptide sequences have been identified in the respective cDNA sequence. Although the protein sequence data is from the bovine protein and the cDNA sequences are human, the sequences are highly homologous (identities: α-subunit 43/50; β-subunit 64/64; γ-subunit 30/32), confirming the cloned cDNAs represent the human homologs of the bovine GlcNAc-phosphotransferase subunits. The α- and β-subunits were found to be encoded by a single cDNA whose gene is on chromosome 12. The γ-subunit is the product of a second gene located on chromosome 16. The α/β-subunits precursor gene has been cloned and sequenced. The gene spans ~80 kb and contains 21 exons. The γ-subunit gene has also been identified in data reported from a genome sequencing effort. The γ-subunit gene is arranged as 11 exons spanning 12 kb of genomic DNA.

Using the human cDNAs, the homologous murine cDNAs for the α-, β- and γ-subunits were isolated and sequenced using standard techniques. The murine α- β-subunit precursor cDNA is shown in SEQ ID NO:16. The deduced amino acid sequence for the murine α-subunit is shown in SEQ ID NO: 15 and the β-subunit in SEQ ID NO:8.

The mouse γ-subunit cDNA was isolated from a mouse liver library in λZap II using the γ-human γ-subunit cDNA as a probe. The human γ-subunit cDNA was random hexamer-labeled with ^{32}P-dCTP and used to screen a mouse liver cDNA library in λZap II. The probe hybridized to three of 500,000 plaques screened. Each was subcloned to

homogeneity, the insert excised, cloned into pUC19, and sequenced using standard methods Sambrook, J., Fritsch E. F., *et al.* (1989). *Molecular Cloning. A Laboratory Manual.* Cold Spring Harbor, Cold Spring Harbor Laboratory Press. The mouse γ-subunit cDNA sequence is shown in SEQ ID NO:10 and the deduced amino acid sequence for the mouse γ-subunit is shown in SEQ ID NO:9.

Comparison of the deduced amino acid sequences of the human and mouse α-, β-, and γ-subunits demonstrates that the proteins are highly homologous with about an 80 percent identity.

To confirm that these enzymes were substantially the same between species, a partial homologous rat cDNA for the α- and β-subunits was isolated and sequenced using standard techniques. The partial rat α- and β-subunit cDNA is shown in SEQ ID NO:12. The deduced amino acid sequence corresponding to the cDNA is shown in SEQ ID NO:11. Further, a partial homologous Drosophila cDNA for the α-and β-subunits was isolated and sequenced using standard techniques. The partial Drosophila α- and β-subunit cDNA is shown in SEQ ID NO:17. The deduced amino acid sequence corresponding to the cDNA is shown in SEQ ID NO:13. Comparisons of the deduced amino acid sequences of the partial human, rat, and Drosophila α- and β-subunits show that the proteins are highly homologous.

Phosphodiester α-GlcNAcase

In another aspect, the present invention provides isolated and purified biologically active phosphodiester α-GlcNAcase, nucleic acid molecules encoding phosphodiester α-GlcNAcase, expression vectors having a DNA that encodes phosphodiester α-GlcNAcase, host cells that have been transfected or transformed with expression vectors having DNA that encodes phosphodiester α-GlcNAcase, methods for producing recombinant phosphodiester

α-GlcNAcase by culturing host cells that have been transfected or transformed with expression vectors having DNA that encodes phosphodiester α-GlcNAcase, isolated and purified recombinant phosphodiester α-GlcNAcase, and methods for using phosphodiester α-GlcNAcase for the preparation of highly phosphorylated lysosomal enzymes that are useful for the treatment of lysosomal storage diseases.

To obtain isolated and purified phosphodiester α-GlcNAcase and the nucleic acid molecules encoding the enzyme according to the present invention, bovine phosphodiester α GlcNAcase was obtained and analyzed as follows. Mice were immunized with a partially purified preparation of phosphodiester α-GlcNAcase and a functional screening strategy was utilized to identify and isolate a monoclonal antibody specific for phosphodiester α-GlcNAcase. Immunogen was prepared by partially purifying phosphodiester α-GlcNAcase ~6000-fold from a bovine pancreas membrane pellet using chromatography on DEAE-Sepharose, iminodiacetic acid Sepharose, and Superose 6. Two BALB/c mice were each injected intraperitoneally with 5 μg partially purified phosphodiester α-GlcNAcase emulsified in Freunds complete adjuvant. On day 28, the mice were boosted intraperitoneally with 5 μg phosphodiester α-GlcNAcase emulsified in Freunds incomplete adjuvant. On day 42 the mice were bled and an phosphodiester α-GlcNAcase specific immune response was documented by "capture assay." To perform the capture assay, serum (5 μl) was incubated overnight with 1.2 units partially purified phosphodiester α-GlcNAcase. Mouse antibody was then captured on rabbit antimouse IgG bound to protein A-Ultralink™ resin. Following extensive washing, bound phosphodiester α-GlcNAcase was determined in the Ultralink pellet by assay of cleavage of [^{3}H]-GlcNAc-l-phosphomannose α-methyl.

Following a second intravenous boost with phosphodiester α-GlcNAcase, the spleen was removed and splenocytes fused with SP2/0 myeloma cells according to our

modifications (Bag, M., Booth J. L., *et al.* (1996). "Bovine UDP-N-acetylglucosamine: lysosomal enzyme N-acetylglucosamine-1-phosphotransferase. I. Purification and subunit structure." *Journal of Biological Chemistry* 271: 31437 - 31445) of standard techniques; Harlow, E. and Lane, D. (1988). *Antibodies: a laboratory manual,* Cold Spring Harbor Laboratory). The fusion was plated in eight 96-well plates in media supplemented with recombinant human IL-6 (Bazin, R. and Lemieux, R. (1989). "Increased proportion of B cell hybridomas secreting monoclonal antibodies of desired specificity in cultures containing macrophage-derived hybridoma growth factor (IL-6)." *Journal of Immunological Methods* 116: 245 - 249) and grown until hybridomas were just visible. Forty-eight pools of 16-wells were constructed and assayed for antiphosphodiester α-GlcNAcase activity using the capture assay. Four pools were positive. Subpools of 4-wells were then constructed from the wells present in the positive 16-well pools. Three of the four 16-well pools contained a single 4-well pool with anti-phosphodiester α-GlcNAcase activity. The 4 single wells making up the 4-well pools were then assayed individually identifying the well containing the anti-phosphodiester α-GlcNAcase secreting hybridomas. Using the capture assay, each hybridoma was subcloned twice and antibody prepared by ascites culture. Monoclonals UC2 and UC3 were found to be low affinity antibodies. UC1, a high affinity IgG monoclonal antibody, was prepared by ascites culture and immobilized on Emphaze for purification of phosphodiester α-GlcNAcase. The monoclonal antibody labeled UC1 was selected for use in further experiments. A hybridoma secreting monoclonal antibody UC1 was deposited with the American Type Culture Collection, 10801 Univerisity Blvd., Manassas, VA 20110 and assigned ATCC Accession No. _____.

To purify phosphodiester α-GlcNAcase, a solubilized membrane fraction was prepared from bovine liver. Phosphodiester α-GlcNAcase was absorbed to monoclonal

antibody UC1 coupled to Emphaze resin by incubation overnight with gentle rotation. The UC1-Emphaze was then packed in a column, washed sequentially with EDTA and $NaHCO_3$ at pH 7.0, then phosphodiester α-GlcNAcase was eluted with $NaHCO_3$ at pH 10. Fractions containing phosphodiester α-GlcNAcase at specific activities >50,000 μ/mg were pooled and adjusted to pH 8.0 with 1/5th volume of 1 M Tris HCl, pH 7.4. Following chromatography on UCI-Emphaze the phosphodiester α-GlcNAcase was purified 92,500-fold in 32% yield.

The phosphodiester α-GlcNAcase from UC1-Emphaze was concentrated and chromatographed on Superose 6. Phosphodiester α-GlcNAcase eluted early in the chromatogram as a symmetric activity peak with a coincident protein peak. Following chromatography on Superose 6, the enzyme was purified ~715,000-fold in 24% yield. The purified enzyme catalyzed the cleavage of 472 μmols/hr/mg [^{3}H]-GlcNAc-l-phosphomannose-α-methyl, corresponding to a specific activity of 472,000 units/mg.

The purified phosphodiester α-GlcNAcase was subjected to SDS-PAGE and protein was detected by silver staining (Blum, H., Beier H., *et al.* (1987). "Improved silver staining of plant proteins, RNA and DNA in polyacrylamide gels." *Electrophoresis:* 93-99). A diffuse band was observed with a molecular mass of approximately 70 kDa whose intensity varies with the measured phosphodiester α-GlcNAcase activity. The diffuse appearance of the band suggests the protein may be heavily glycosylated. A faint band with a molecular mass of ~150,000, which does not correlate with activity, was also present.

A model for the subunit structure of phosphodiester α-GlcNAcase was determined by gel filtration chromatography and SDS-PAGE with and without disulfide bond reduction. The mass by gel filtration is about 300,000. SDS-PAGE without disulfide bond reduction is ~140,000. Following disulfide bond reduction, the apparent mass is 70,000. Together these data show phosphodiester α-GlcNAcase is a tetramer composed of disulfide linked

homodimers. Figure 2 shows a model of the subunit structure of phosphodiester α-GlcNAcase.

The amino terminal amino acid sequence of affinity purified, homogeneous bovine phosphodiester α-GlcNAcase was determined using standard methods (Matsudaira, P., Ed. (1993). *A Practical Guide to Protein and Peptide Purification for Microsequencing*. San Diego, Academic Press, Inc.). The pure enzyme was also subjected to trypsin digestion and HPLC to generate two internal tryptic peptides which were sequenced. The amino acid sequences of these three peptides are:

Peptide 1 - Amino Terminal DXTRVHAGRLEHESWPPAAQTAGAHRPSVRTFV (SEQ ID NO:23);

Peptide 2 - Tryptic RDGTLVTGYLSEEEVLDTEN (SEQ ID NO:24): and

Peptide 3 - Tryptic GINLWEMAEFLLK (SEQ ID NO:25).

The protein, nucleotide, and EST data bases were searched for sequences that matched these peptide sequences and several human and mouse ESTs were found that had the sequence of the third peptide at their amino termini. Three human infant brain EST clones and one mouse embryo clone were obtained from ATCC and sequenced. The three human clones were all identical except for total length at their 3' ends and virtually identical to the mouse clone, except that the mouse EST contained a 102 bp region that was absent from all three human brain ESTs. An EcoR I -Hind III fragment of about 700 bp was excised from the human cDNA clone (ATCC # 367524) and used to probe a human liver cDNA library directionally cloned in TriplEx vector (Clontech). Of the positive clones isolated from the library and converted to plasmids (pTriplEx), the largest (2200 bp) was represented by clone 6.5 which was used for the rest of the analysis.

The cDNA clone has been completely sequenced on both strands and is a novel

sequence that predicts a mature protein of about 50 kDa which is in agreement with the size of the deglycosylated mature bovine liver phosphodiester α-GlcNAcase.

There is a unique BamH I site at base #512 and a unique Hind ID site at base # 1581. All three bovine peptide sequences (peptides 1, 2, and 3) were found. Although the sequences of peptides 2 and 3 in the human are 100% identical to the bovine sequences, the amino-terminal peptide in humans is only 67% identical to the bovine sequence. The human liver clone contains the 102 base pair insert that has the characteristics of an alternatively spliced segment that was missing in the human brain EST. The hydrophilicity plot indicates the presence of a hydrophobic membrane spanning region from amino acids 448 to 474 and another hydrophobic region from amino acid 8 to 24 which fits the motif for a signal sequence and there is a likely signal sequence cleavage site between G24 and G25. There are six Asn-X-Ser/Thr potential N-linked glycosylation sites, one of which is within the 102 bp insert. All of these sites are amino terminal of the putative trans-membrane region. These features indicate that the phosphodiester α-GlcNAcase is a type I membrane spanning glycoprotein with the amino terminus in the lumen of the Golgi and the carboxyl terminus in the cytosol. This orientation is different from that of other glycosyltransferases and glycosidases involved in glycoprotein processing, which to date have been shown to be type II membrane spanning proteins.

The amino acid sequence for the phosphodiester α-GlcNAcase monomer is shown in amino acids 50-515 of SEQ ID NO:6. The signal peptide is shown in amino acids 1-24 of SEQ ID NO:6 and the pro segment is shown in amino acids 25-49 of SEQ ID NO:6. The human cDNA was cloned using the techniques described above. The nucleotide sequence for the monomer that associates to form the phosphodiester α-GlcNAcase tetramer is shown in nucleotides 151-1548 of SEQ ID NO:7. The nucleotide sequence for the signal sequence

is shown in nucleotides 1-72 of SEQ ID NO:7. The nucleotide sequence for the propeptide is shown in nucleotides 73-150 of SEQ ID NO:7.

The murine cDNA for phosphodiester α-GlcNAcase is shown in SEQ ID NO:18. The deduced amino acid sequence for the murine phosphodiester α-GlcNAcase is shown in SEQ ID NO:19. Comparison of the deduced amino acid sequences of the human and mouse enzymes demonstrates that the proteins are highly homologous with about an 80 percent identity. This is especially true in the region of the active site where identity exceeds 90%. The murine gene for phosphodiester α-GlcNAcase is shown in SEQ ID NO:14.

The human phosphodiester α-GlcNAcase gene has been identified by database searching. The sequence was determined during the sequencing of clone l65E7 from chromosome 16.13.3, GenBank AC007011.1, gi4371266. Interestingly, the phosphodiester α-GlcNAcase gene was not identified by the SCAN program used to annotate the sequence.

Because of the degeneracy of the genetic code, a DNA sequence may vary from that shown in SEQ ID NO:4, SEQ ID NO:5, and SEQ ID NO:7 and still encode a GlcNAc phosphotransferase and a phosphodiester α-GlcNAcase enzyme having the amino acid sequence shown in SEQ ID NO: 1, SEQ ID NO:2, SEQ ID NO:3, and SEQ ID NO:6. Such variant DNA sequences may result from silent mutations, e.g., occurring during PCR amplification, or may be the product of deliberate mutagenesis of a native sequence. The invention, therefore, provides equivalent isolated DNA sequences encoding biologically active GlcNAc-phosphotransferase and phosphodiester α-GlcNAcase selected from: (a) the coding region of a native mammalian GlcNAc-phosphotransferase gene and phosphodiester α-GlcNAcase gene; (b) cDNA comprising the nucleotide sequence presented in SEQ ID NO:4, SEQ ID NO:5, and SEQ ID NO:7; (c) DNA capable of hybridization to the native mammalian GlcNAc-phosphotransferase gene and phosphodiester α-GlcNAcase gene under

moderately stringent conditions and which encodes biologically active GlcNAc-phosphotransferase and phosphodiester α-GlcNAcase; and (d) DNA which is degenerate as a result of the genetic code to a DNA defined in (a), (b), or (c) and which encodes biologically active GlcNAc-phosphotransferase and phosphodiester α-GlcNAcase. GlcNAc-phosphotransferase and phosphodiester α-GlcNAcase proteins encoded by such DNA equivalent sequences are encompassed by the invention.

Those sequences which hybridize under stringent conditions and encode biologically functional GlcNAc-phosphotransferase and phosphodiester α-GlcNAcase are preferably at least 50-100% homologous, which includes 55, 60, 65, 70, 75,75, 80, 85, 90, 95, 99% and all values and subranges therebetween. Homology may be determined with the software UWCG as described above. Stringent hybridization conditions are known in the art and are meant to include those conditions which allow hybridization to those sequences with a specific homology to the target sequence. An example of such stringent conditions are hybridization at 65°C in a standard hybridization buffer and subsequent washing in 0.2 X concentrate SSC and 0.1% SDS at 42-65°C, preferably 60°C. This and other hybridization conditions are disclosed in Sarnbrook, J., Fritsch E. F., *et al.* (1989). *Molecular Cloning. A Laboratory Manual.* Cold Spring Harbor, Cold Spring Harbor Laboratory Press. Alternatively, the temperature for hybridization conditions may vary dependent on the percent GC content and the length of the nucleotide sequence, concentration of salt in the hybridization buffer and thus the hybridization conditions may be calculated by means known in the art.

Recombinant Expression for GlcNAc-phosphotransferase and Phosphodiester α-GlcNAcase Isolated and purified recombinant GlcNAc-phosphotransferase and phosphodiester α-GlcNAcase enzymes are provided according to the present invention by

incorporating the DNA corresponding to the desired protein into expression vectors and expressing the DNA in a suitable host cell to produce the desired protein.

Expression Vectors

Recombinant expression vectors containing a nucleic acid sequence encoding the enzymes can be prepared using well known techniques. The expression vectors include a DNA sequence operably linked to suitable transcriptional or translational regulatory nucleotide sequences such as those derived from mammalian, microbial, viral, or insect genes. Examples of regulatory sequences include transcriptional promoters, operators, enhancers, mRNA ribosomal binding sites, and appropriate sequences which control transcription and translation initiation and termination. Nucleotide sequences are "operably linked" when the regulatory sequence functionally relates to the DNA sequence for the appropriate enzyme. Thus, a promoter nucleotide sequence is operably linked to a GlcNAc-phosphotransferase or phosphodiester a GlcNAcase DNA sequence if the promoter nucleotide sequence controls the transcription of the appropriate DNA sequence.

The ability to replicate in the desired host cells, usually conferred by an origin of replication and a selection gene by which transformants are identified, may additionally be incorporated into the expression vector.

In addition, sequences encoding appropriate signal peptides that are not naturally associated with GlcNAc-phosphotransferase or phosphodiester α-GlcNAcase can be incorporated into expression vectors. For example, a DNA sequence for a signal peptide (secretory leader) may be fused in-frame to the enzyme sequence so that the enzyme is initially translated as a fusion protein comprising the signal peptide. A signal peptide that is functional in the intended host cells enhances extracellular secretion of the appropriate

polypeptide. The signal peptide may be cleaved from the polypeptide upon secretion of enzyme from the cell.

Host Cells

Suitable host cells for expression of GlcNAc-phosphotransferase and phosphodiester at α-GlcNAcase include prokaryotes, yeast, archae, and other eukaryotic cells. Appropriate cloning and expression vectors for use with bacterial, fungal, yeast, and mammalian cellular hosts are well known in the art, *e.g.,* Pouwels *et al.* Cloning Vectors: A Laboratory Manual, Elsevier, New York (1985). The vector may be a plasmid vector, a single or double-stranded phage vector, or a single or double-stranded RNA or DNA viral vector. Such vectors may be introduced into cells as polynucleotides, preferably DNA, by well known techniques for introducing DNA and RNA into cells. The vectors, in the case of phage and viral vectors also may be and preferably are introduced into cells as packaged or encapsulated virus by well known techniques for infection and transduction. Viral vectors may be replication competent or replication defective. In the latter case viral propagation generally will occur only in complementing host cells. Cell-free translation systems could also be employed to produce the enzymes using RNAs derived from the present DNA constructs.

Prokaryotes useful as host cells in the present invention include gram negative or gram positive organisms such as E. *coli* or *Bacilli.* In a prokaryotic host cell, a polypeptide may include a N-terminal methionine residue to facilitate expression of the recombinant polypeptide in the prokaryotic host cell. The N-terminal Met may be cleaved from the expressed recombinant GlcNAc-phosphotransferase or phosphodiester α-GlcNAcase polypeptide. Promoter sequences commonly used for recombinant prokaryotic host cell expression vectors include β-lactamase and the lactose promoter system.

Expression vectors for use in prokaryotic host cells generally comprise one or more phenotypic selectable marker genes. A phenotypic selectable marker gene is, for example, a gene encoding a protein that confers antibiotic resistance or that supplies an autotrophic requirement. Examples of useful expression vectors for prokaryotic host cells include those derived from commercially available plasmids such as the cloning vector pBR322 (ATCC 37017). pBR322 contains genes for ampicillin and tetracycline resistance and thus provides simple means for identifying transformed cells. To construct an expression vector using pBR322, an appropriate promoter and a DNA sequence are inserted into the pBR322 vector.

Other commercially available vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and pGEM1 (Promega Biotec, Madison, Wisconsin., USA).

Promoter sequences commonly used for recombinant prokaryotic host cell expression vectors include β-lactamase (penicillinase), lactose promoter system (Chang *et al.*, Nature275:615, (1978); and Goeddel *et al.*, Nature 281:544, (1979)), tryptophan (trp) promoter system (Goeddel *et al.*, Nucl. Acids Res. 8:4057, (1980)), and tac promoter (Maniatis, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, p. 412 (1982)).

Yeasts useful as host cells in the present invention include those from the genus Saccharomyces, Pichia, K. Actinomycetes and Kluyveromyces. Yeast vectors will often contain an origin of replication sequence from a 2μ yeast plasmid, an autonomously replicating sequence (ARS), a promoter region, sequences for polyadenylation, sequences for transcription termination, and a selectable marker gene. Suitable promoter sequences for yeast vectors include, among others, promoters for metallothionein, 3-phosphoglycerate kinase (Hitzeman *et al.*, J. Biol. Chem. 255:2073, (1980)) or other glycolytic enzymes

(Holland *et al.*, Biochem. 17:4900, (1978)) such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvatee decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase. Other suitable vectors and promoters for use in yeast expression are further described in Fleer *et al.*, Gene, 107:285-195 (1991). Other suitable promoters and vectors for yeast and yeast transformation protocols are well known in the art.

Yeast transformation protocols are known to those of skill in the art. One such protocol is described by Hinnen *et al., Proceedings of the National Academy of Sciences USA,* 75:1929 (1978). The Hinnen protocol selects for Trp.sup.+ transformants in a selective medium, wherein the selective medium consists of 0.67% yeast nitrogen base, 0.5% casamino acids, 2% glucose, 10 μg/ml adenine, and 20 μg/ml uracil.

Mammalian or insect host cell culture systems well known in the art could also be employed to express recombinant GlcNAc-phosphotransferase or phosphodiester α-GlcNAcase polypeptides, *e.g.*, Baculovirus systems for production of heterologous proteins in insect cells (Luckow and Summers, Bio/Technology 6:47 (1988)) or Chinese hamster ovary (CHO) cells for mammalian expression may be used. Transcriptional and translational control sequences for mammalian host cell expression vectors may be excised from viral genomes. Commonly used promoter sequences and enhancer sequences are derived from Polyoma virus, Adenovirus 2, Simian Virus 40 (SV40), and human cytomegalovirus. DNA sequences derived from the SV40 viral genome may be used to provide other genetic elements for expression of a structural gene sequence in a mammalian host cell, *e.g.*, SV40 origin, early and late promoter, enhancer, splice, and polyadenylation sites. Viral early and late promoters are particularly useful because both are easily obtained from a viral genome

as a fragment which may also contain a viral origin of replication. Exemplary expression vectors for use in mammalian host cells are well known in the art.

The enzymes of the present invention may, when beneficial, be expressed as a fusion protein that has the enzyme attached to a fusion segment. The fusion segment often aids in protein purification, *e.g.*, by permitting the fusion protein to be isolated and purified by affinity chromatography. Fusion proteins can be produced by culturing a recombinant cell transformed with a fusion nucleic acid sequence that encodes a protein including the fusion segment attached to either the carboxyl and/or amino terminal end of the enzyme. Preferred fusion segments include, but are not limited to, glutathione-S-transferase, β-galactosidase, a poly-histidine segment capable of binding to a divalent metal ion, and maltose binding protein. In addition, the HPC-4 epitope purification system may be employed to facilitate purification of the enzymes of the present invention. The HPC-4 system is described in U.S. Patent No. 5,202,253, the relevant disclosure of which is herein incorporated by reference.

Expression by gene activation technology

In addition to expression strategies involving transfection of a cloned cDNA sequence, the endogenous GlcNAc-phophotransfease and phosphodiester α-GlcNAcase genes can be expressed by altering the promoter.

Methods of producing the enzymes of the present invention can also be accomplished according to the methods of protein production as described in U.S. Patent No. 5,968,502, the relevant disclosure of which is herein incorporated by reference, using the sequences for GlcNAc-phosphotransferase and phosphodiester α-GlcNAcase as described herein.

Expression and Recovery

According to the present invention, isolated and purified GlcNAc-phosphotransferase or phosphodiester α-GlcNAcase enzymes may be produced by the recombinant expression systems described above. Thc method comprises culturing a host cell transformed with an expression vector comprising a DNA sequence that encodes the enzyme under conditions sufficient to promote expression of the enzyme. The enzyme is then recovered from culture medium or cell extracts, depending upon the expression system employed. As is known to the skilled artisan, procedures for purifying a recombinant protein will vary according to such factors as the type of host cells employed and whether or not the recombinant protein is secreted into the culture medium. When expression systems that secrete the recombinant protein are employed, the culture medium first may be concentrated. Following the concentration step, the concentrate can be applied to a purification matrix such as a gel filtration medium. Alternatively, an anion exchange resin can be employed, *e.g.*, a matrix or substrate having pendant diethylaminoethyl (DEAE) groups. The matrices can be acrylamide, agarose, dextran, cellulose, or other types commonly employed in protein purification. Also, a cation exchange step can be employed. Suitable cation exchangers include various insoluble matrices comprising sulfopropyl or carboxymethyl groups. Further, one or more reversed-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media *(e.g.*, silica gel having pendant methyl or other aliphatic groups) can be employed to further purify the enzyme. Some or all of the foregoing purification steps, in various combinations, are well known in the art and can be employed to provide an isolated and purified recombinant protein.

Recombinant protein produced in bacterial culture is usually isolated by initial disruption of the host cells, centrifugation, extraction from cell pellets if an insoluble

polypeptide, or from the supernatant fluid if a soluble polypeptide, followed by one or more concentration, salting-out, ion exchange, affinity purification, or size exclusion chromatography steps. Finally, RP-HPLC can be employed for final purification steps. Microbial cells can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Preparation of Highly Phosphorylated Lysosomal Enzymes

In another aspect, the present invention provides highly phosphorylated lysosomal hydrolases and methods for the preparation of such hydrolases. The highly phosphorylated lysosomal hydrolases can be used in clinical applications for the treatment of lysosomal storage diseases.

The method comprises obtaining lysosomal hydrolases having asparagine-linked oligosaccharides with high mannose structures and modifying the α1,2-linked or other outer mannoses by the addition of M6P *in vitro* to produce a hydrolase that can be used for the treatment of lysosomal storage diseases because it binds to cell membrane M6P receptors and is readily taken into the cell and into the lysosome. Typically, the high mannose structures consist of from six to nine molecules of mannose and two molecules of N-acetylglucosamine (GlcNAc). In the preferred embodiment, the high mannose structure is a characteristic MAN7(D_2D_3) isomer structure consisting of seven molecules of mannose and two molecules of N-acetylglucosamine (GlcNAc).

Highly phosphorylated Lysosomal hydrolases are produced by treating the high mannose hydrolases with GlcNAc-phosphotransferase which catalyzes the transfer of N-acetylglucosamine-1-phosphate from UDP-GlcNAc to the 6' position of α1,2-linked or other outer mannoses on the hydrolase. This GlcNAc-phosphotransferase modified hydrolase is

then treated with phosphodiester α-GlcNAcase which catalyz
Acetylglucosamine to generate terminal M6P on the hydrolase.

In one embodiment of the invention, the GlcNAc-phosphotransferase treated hydrolase may be isolated and stored without any subsequent treatment. Subsequently, the GlcNAc-phosphotransferase treated hydrolase may be modified further by treating the hydrolase with a phosphodiester α-GlcNAcase.

Surprisingly, it has been found that the hydrolases containing M6P generated by this method are highly phosphorylated when compared to naturally occurring or known recombinant hydrolases. The highly phosphorylated lysosomal hydrolases of the present invention contain from about 6% to about 100% bis-phosphorylated oligosaccharides compared to less that about 5% bis-phosphorylated oligosaccharides on known naturally occurring or recombinant hydrolases.

These highly phosphorylated hydrolases have a higher affinity for the M6P receptor and are therefore more efficiently taken into the cell by plasma membrane receptors. (Reuser, A. J., Kroos, M. A., Ponne, N. J., Wolterman, R. A., Loonen, M. C., Busch, H. F., Visser, W. J., and Bolhuis, P. A. (1984). "Uptake and stability of human and bovine acid alpha-glucosidase in cultured fibroblasts and skeletal muscle cells from glycogenosis type II patients." *Experimental Cell Research* 155: 178-189).

The high-affinity ligand for the cation-independent M6P receptor is an oligosaccharide containing two M6P groups *(i.e.,* a bis-phosphorylated oligosaccharide). Since a bisphosphorylated oligosaccharides binds with an affinity 3500-fold higher than a monophosphorylated oligosaccharides, virtually all the high-affinity binding of a lysosomal enzyme to the M6P receptor will result from the content of bis-phosphorylated oligosaccharides (Tong, P. Y., Gregory, W., and Kornfeld, S. (1989)). "Ligand interactions

of the cation-independent mannose 6-phosphate receptor. The stoichiometry of mannose 6-phosphate binding." *Journal of Biological Chemistry* 264: 7962-7969). It is therefore appropriate to use the content of bis-phosphorylated oligosaccharides to compare the binding potential of different preparations of lysosomal enzymes.

The extent of mannose 6-phosphate modification of two different lysosomal enzymes has been published. The oligosaccharide composition of human α-galactosidase A secreted from Chinese hamster ovary cells has been published (Matsuura, F., Ohta, M., Ioannou, Y. A., and Desnick, R. I. (1998). "Human alpha-galactosidase A: characterization of the N-linked oligosaccharides on the intracellular and secreted glycoforms overexpressed by Chinese hamster ovary cells." *Glycobiology 8(4):* 329-39). Of all oligosaccharides on α-gal A released by hydrazinolysis, only 5.2% were bis-phosphorylated. Zhao *et al.* partially characterized the oligosaccharide structures on recombinant human α-iduronidase secreted by CHO cells (Zhao, K. W., Faull, K. F., Kakkis, E. D., and Neufeld, E. F. (1997). "Carbohydrate structures of recombinant human alpha-L-iduronidase secreted by Chinese hamster ovary cells." J *Biol Chem* 272(36): 22758-65) and demonstrated a minority of the oligosaccharides were bisphosphorylated. The qualitative techniques utilized precluded the determination of the fraction of oligosaccharides phosphorylated.

The production and secretion of human acid α-glucosidase by CHO cells has been reported (Van Hove, J. L., Yang, H. W., Wu, J. Y., Brady, R. O., and Chen, Y. T. (1996). "High level production of recombinant human lysosomal acid alpha-glucosidase in Chinese hamster ovary cells which targets to heart muscle and corrects glycogen accumulation in fibroblasts from patients with Pompe disease." *Proceedings of the National Academy of Sciences USA, 93(1): 6570*). The carbohydrate structures of this preparation were not characterized in this publication. However, this preparation was obtained and analyzed. The

results, given in the examples below, showed that less than 1% of the oligosaccharides contained any M6P and bis-phosphorylated oligosaccharides were not detectable. Together, these data show that known preparations of recombinant lysosomal enzymes contain no more than 5.2% phosphorylated oligosaccharides. It appears that the preparation of more highly phosphorylated lysosomal enzymes is unlikely to be achieved with known techniques. Naturally occurring human acid α-glucosidase purified from human placenta contains very low levels of M6P (Mutsaers, I. H. G. M., Van Halbeek, H., Vliegenthart, J. F. G., Tager, J. M., Reuser, A. J. J., Kroos, M., and Galjaard, H. (1987). "Determination of the structure of the carbohydrate chains of acid α-glucosidase from human placenta." *Biochimica et Biophysica Acta* 911: 244 - 251). The arrangement of the phosphates as either bis- or monophosphorylated oligosaccharides has not been determined, but less than 1% of the oligosaccharides contain any M6P.

The highly phosphorylated hydrolases of the present invention are useful in enzyme replacement therapy procedures because they are more readily taken into the cell and the lysosome. (Reuser, A. J., Kroos, M. A., Ponne, N. J., Wolterman, R. A., Loonen, M. C., Busch, H. F., Visser, W. J. and Bolhuis, P. A. (1984). "Uptake and stability of human and bovine acid alpha-glucosidase in cultured fibroblasts and skeletal muscle cells from glycogenosis type II patients." *Experimental Cell Research* 155: 178-189).

Any lysosomal enzyme that uses the M6P transport system can be treated according to the method of the present invention. Examples include α-glucosidase (Pompe Disease), α–L-iduronidase (Hurler Syndrome), α-galactosidase A (Fabry Disease), arylsulfatase (Maroteaux-Lamy Syndrome), N-acetylgalactosamine-6-sulfatase or β-galactosidase (Morquio Syndrome), iduronate 2-sulfatase (Hunter Syndrome), ceramidase (Farber Disease), galactocerebrosidase (Krabbe Disease), β-glucuronidase (Sly Syndrome), Heparan

N-sulfatase (Sanfilippo A), N-Acetyl-α-glucosaminidase (Sanfilippo B), Acetyl CoA-α-glucosaminide N-acetyl transferase, N-acetyl-glucosamine-6 sulfatase (Sanfilippo D), Galactose 6-sulfatase (Morquio A), Arylsulfatase A, B, and C (Multiple Sulfatase Deficiency), Arylsulfatase A Cerebroside (Metachromatic Leukodystrophy), Ganglioside (Mucolipidosis IV), Acid β-galactosidase G_{M1} Galglioside (G_{M1} Gangliosidosis), Acid β-galactosidase (Galactosialidosis), Hexosaminidase A (Tay-Sachs and Variants), Hexosaminidase B (Sandhoff), α-fucosidase (Fucsidosis), α-N-Acetyl galactosaminidase (Schindler Disease), Glycoprotein Neuraminidase (Sialidosis), Aspartylglucosamine amidase (Aspartylglucosaminuria), Acid Lipase (Wolman Disease), Acid Ceramidase (Farber Lipogranulomatosis), Lysosomal Sphingomyelinase and other Sphingomyelinase (Nieman-Pick).

Methods for treating any particular lysosomal hydrolase with the enzymes of the present invention are within the skill of the artisan. Generally, the lysosomal hydrolase at a concentration of about 10 mg/ml and GlcNAc-phosphotransferase at a concentration of about 100,000 units/mL are incubated at about 37°C for 2 hours in the presence of a buffer that maintains the pH at about 6-7 and any stabilizers or coenzymes required to facilitate the reaction. Then, phosphodiester α-GlcNAcase is added to the system to a concentration of about 1000 units/mL and the system is allowed to incubate for about 2 more hours. The modified lysosomal enzyme having highly phosphorylated oligosaccharides is then recovered by conventional means.

In a preferred embodiment, the lysosomal hydrolase at 10 mg/ml is incubated in 50 mm Tris-HCl, pH 6.7, 5 mM $MgCl_2$, 5 mM $MnCl_2$, 2 mM UDP-GlcNAc with GlcNAc phosphotransferase at 100,000 units/mL at 37°C for 2 hours. Phosphodiester α-GlcNAcase, 1000 units/mL, is then added and the incubation continued for another 2 hours. The

modified enzyme is then repurified by chromatography on Q-Sepharose and step elution with NaCl.

Methods for Obtaining High Mannose Lysosomal Hydrolases

High mannose lysosomal hydrolases for treatment according to the present invention can be obtained from any convenient source, e.g., by isolating and purifying naturally occurring enzymes or by recombinant techniques for the production of proteins. High mannose lysosomal hydrolases can be prepared by expressing the DNA encoding a particular hydrolase in any host cell system that generates a oligosaccharide modified protein having high mannose structures, *e.g.*, yeast cells, insect cells, other eukaryotic cells, transformed Chinese Hamster Ovary (CHO) host cells, or other mammalian cells.

In one embodiment, high mannose lysosomal hydrolases are produced using mutant yeast that are capable of expressing peptides having high mannose structures. These yeast include the mutant *S. cervesiae Δ ochl, Δ mnnl* (Nakanishi-Shindo, Y., Nakayama, K. I., Tanaka, A., Toda, Y. and Jigami, Y. (1993). "Structure of the N-linked oligosaccharides that show the complete loss of α-1,6-polymannose outer chain from *ochl, ochl mnnl,* and *ochl mnnl alg3* mutants of *Saccharomyces cerevisiae." Journal of Biological Chemistry* 268: 26338 - 26345).

Preferably, high mannose lysosomal hydrolases are produced using over-expressing transformed insect, CHO, or other mammalian cells that are cultured in the presence of certain inhibitors. Normally, cells expressing lysosomal hydrolases secrete acid α-glucosidase that contains predominantly sialylated biantenniary complex type glycans that do not serve as a substrate for GlcNAc-phosphotransferase and therefore cannot be modified to use the M6P receptor.

According to the present invention, a new method has been discovered for manipulating transformed cells containing DNA that expresses a recombinant hydrolase so that the cells secrete high mannose hydrolases that can be modified according to the above method. In this method, transformed cells are cultured in the presence of α1,2-mannosidase inhibitors and the high mannose recombinant hydrolases are recovered from the culture medium. Inhibiting alpha 1,2-mannosidase prevents the enzyme from trimming mannoses and forces the cells to secrete glycoproteins having the high mannose structure. High mannose hydrolases are recovered from the culture medium using known techniques and treated with GlcNAc-phosphotransferase and phosphodiester α-GlcNAcase according to the method herein to produce hydrolases that have M6P and can therefore bind to membrane M6P receptors and be taken into the cell. Preferably, the cells are CHO cells and the hydrolases are secreted with the MAN7(D_2D_3) structure. Figure 3 shows the reaction scheme for this method.

In a preferred embodiment, recombinant human acid alpha glucosidase ("rh-GAA") is prepared by culturing CHO cells secreting rh-GAA in Iscove's Media modified by the addition of an alpha 1,2-mannosidase inhibitor. Immunoprecipitation of rh-GAA from the media followed by digestion with either N-glycanase or endoglycosidase-H demonstrates that in the presence of the alpha 1,2-mannosidase inhibitor the rh-GAA retains high mannose structures rather than the complex structures found on a preparation secreted in the absence of the inhibitor. The secreted rh-GAA bearing high mannose structures is then purified to homogeneity, preferably by chromatography beginning with ion exchange chromatography on ConA-Sepharose, Phenyl-Sepharose and affinity chromatography on Sephadex G-100. The purified rh-GAA is then treated *in vitro* with GlcNAc-phosphotransferase to convert specific mannoses to GlcNAc-phospho-mannose diesters. The GlcNAcphosphomannose

diesters are then converted to M6P groups by treatment with phosphodiester α GlcNAcase. Experiments show that 74% of the rh-GAA oligosaccharides were phosphorylated, 62% being bis-phosphorylated, and 12% monophosphorylated. Since each molecule of rh-GAA contains 7 N-linked oligosaccharides, 100% of the rh-GAA molecules are likely to contain the mannose-phosphate modification.

Any alpha 1,2-mannosidase inhibitor can function in the present invention. Preferably, the inhibitor is selected from the group consisting of deoxymannojirimycin (dMM), kifunensine, D-Mannonolactam amidrazone, and N-butyl-deoxymannojirimycin. Most preferably the inhibitor is deoxymannojimycin.

Treatment of Lysosomal Storage Diseases

In a further aspect, the present invention provides a method for the treatment of lysosomal storage diseases by administering a disease treating amount of the highly phosphorylated lysosomal hydrolases of the present invention to a patient suffering from the corresponding lysosomal storage disease. While dosages may vary depending on the disease and the patient, the enzyme is generally administered to the patient in amounts of from about 0.1 to about 1000 milligrams per 50 kg of patient per month, preferably from about 1 to about 500 milligrams per 50 kg of patient per month. The highly phosphorylated enzymes of the present invention are more efficiently taken into the cell and the lysosome than the naturally occurring or less phosphorylated enzymes and are therefore effective for the treatment of the disease. Within each disease, the severity and the age at which the disease presents may be a function of the amount of residual lysosomal enzyme that exists in the patient. As such, the present method of treating lysosomal storage diseases includes providing the highly phosphorylated lysosomal hydrolases at any or all stages of disease progression.

The lysosomal enzyme is administered by any convenient means. For example, the enzyme can be administered in the form of a pharmaceutical composition containing the enzyme and any pharmaceutically acceptable carriers or by means of a delivery system such as a liposome or a controlled release pharmaceutical composition. The term "pharmaceutically acceptable" refers to molecules and compositions that are physiologically tolerable and do not typically produce an allergic or similar unwanted reaction such as gastric upset or dizziness when administered. Preferably, "pharmaceutically acceptable" means approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopoeia or other generally recognized pharmacopoeia for use in animals, preferably humans. The term "carrier" refers to a diluent, adjuvant, excipient, or vehicle with which the compound is administered. Such pharmaceutical carriers can be sterile liquids, such as saline solutions, dextrose solutions, glycerol solutions, water and oils emulsions such as those made with oils of petroleum, animal, vegetable, or synthetic origin (peanut oil, soybean oil, mineral oil, or sesame oil). Water, saline solutions, dextrose solutions, and glycerol solutions are preferably employed as carriers, particularly for injectable solutions.

The enzyme or the composition can be administered by any standard technique compatible with enzymes or their compositions. For example, the enzyme or composition can be administered parenterally, transdermally, or transmucosally, *e.g.*, orally or nasally. Preferably, the enzyme or composition is administered by intravenous injection.

The following Examples provide an illustration of embodiments of the invention and should not be construed to limit the scope of the invention which is set forth in the appended claims. In the following Examples, all methods described are conventional unless otherwise specified.

EXAMPLES

Materials and Methods

Lactating bovine udders were obtained from Mikkelson Beef, Inc. (Oklahoma City, OK). Ultrasphere ODS columns were obtained from Beckman Instruments. Microsorb MV-NH_2 columns were obtained from Rainin Instrument Co., Inc. (Woburn, MA). [γ^{32}P]ATP (7000 Ci/mmol; end labeling grade), $Na^{125}I$, and Lubrol ($C_{16}H_{33}(CH_2CH_2O)_{23}H$) were obtained from ICN (Costa Mesa, CA). Superose 6 (prep grade), DEAE-Sepharose FF, QAE-Sephadex A-25, molecular mass standards for SDS-PAGE, HiTrap-protein G columns, and Mono Q columns were obtained from Pharmacia Biotech Inc. 3M-Emphaze Biosupport Medium AB1, IODO GEN iodination reagent, and the BCA protein assay reagent were obtained from Pierce. Glycerol, sucrose, α-methylmannoside, α-methylglucoside, reactive green 19-agarose, sodium deoxycholate, benzamidine, UDP-GlcNAc, phenylmethylsulfonyl fluoride, Tris, rabbit anti-mouse IgG, and mouse monoclonal antibody isotyping reagents were obtained from Sigma.

POROS 50 HQ was obtained from PerSeptive Biosystems (Cambridge, MA). ProBlott polyvinylidene difluoride membranes were obtained from Applied Biosystems Inc. (Foster City, CA). A Model QT12 rotary tumbler was obtained from LORTONE, Inc. (Seattle, WA). A mouse immunoglobulin standard panel was obtained from Southern Biotechnology Associates, Inc. (Birmingham, AL). Recombinant interleukin-6, porcine uteroferrin, and monoclonal antibody BP95 were gifts from colleagues. Other chemicals were reagent grade or better and were from standard suppliers.

Example 1

Preparation of monoclonal antibodies specific for bovine GlcNAc-phosphotransferase

Bovine GlcNAc-phosphotransferase was partially purified 30,000 fold as described

(Bao, M., Booth J. L., *et al.* (1996). "Bovine UDP-N-acetylglucosamine: Lysosomal enzyme N-acetylglucosamine-1-phosphotransferase. I. Purification and subunit structure." *Journal of Biological Chemistry* 271: 31437 - 31445) and used to immunize mice. Spleens of immune mice were removed and spenocytes fused with SP2/0 myeloma cells according to Harlow (Harrow, E. and Lane, D. *(1988). Antibodies: a laboratory manual,* Cold Spring Harbor Laboratory). The fusion was plated into 96 well plates and cultured in HAT media until hybridomas were visible.

Hybridomas secreting monoclonal antibodies capable of capturing GlcNAc-phosphotransferase from a crude sample were identified by incubation of hybridoma media (200 µl) with 200 units. Partially purified GlcNAc-phosphotransferase and capturing the resulting immune complex on rabbit anti-mouse IgG bound to protein A coupled to Ultralink™ matrix. Immune complexes which contained monoclonal antibodies directed against GlcNAc-phosphotransferase were then identified by assay of the immune complex for GlcNAc-phosphotransferase activity. By this strategy, four monoclonals directed against GlcNAc-phosphotransferase were identified in the fifth fusion screened. The hybridomas identified were subcloned twice using the same assay and ascites was produced in BALBc mice according to standard techniques (Harlow, E. and Lane, D. (1988). *Antibodies: a laboratory manual,* Cold Spring Harbor Laboratory). The monoclonal antibody labeled PT18 was selected for use in further experiments.

Example 2

Purification of bovine GlcNAc-phosphotransferase

Lactating bovine mammary gland (6 kg) was collected at slaughter and immediately sliced into 10 cm thick slices and chilled in ice. Following homogenization in a Waring commercial blender, the post-nuclear supernatant fraction was prepared by centrifugation.

Membrane fragments were collected by high speed centrifugation (39,000 x g, 45 minutes) and membrane proteins were solubilized in 4% Lubrol, 0.5 % deoxycholate. GlcNAc-phosphotransferase was specifically adsorbed from the solubilized membrane fraction by incubation ovemight with 10 ml of monoclonal antibody PT18 coupled to Ultralink™ matrix (substitution 5 mg/ml). The matrix was then collected by low speed centrifugation, washed with 0.025 M Tris-HCI, pH 7.4, 0.005 M $MgCl_2$, 0.3 % Lubrol buffer containing 1 M NaCI. The column was then washed with 2 column volumes of 0.01 M Tris-HCI, pH 7.4, 0.005 M MgCl2, 0.3 % Lubrol buffer. GlcNAc-phosphotransferase was then eluted from the column with 0.10 M Tris-HCl, pH 10.0, 0.005 M MgCl2, 0.3 % Lubrol and neutralized with 1/10th volume of 1 M Tris-HCI, pH 6.0. Recovery is typically 20-50% of the GlcNAc-phosphotransferase activity present in the homogenized tissue, and approximately 0.5 mg of enzyme is recovered per 10 kg of tissue processed.

Example 3

Amino acid sequencing of bovine GlcNAc-phosphotransferase

Example 3A

Reduction, alkylation and separation of individual subunits

Bovine GlcNAc-phosphotransferase, 1.9 mg was desalted on a column of Sephadex G-25 superfine equilibrated in 9% formic acid and lyophilized. The lyophilized protein was dissolved in 1 ml of 500 mM Tris-HCI, pH 8.6, 6 M guanidine-HCI, 10 mM EDTA, 2 mM DTT degassed by bubbling N_2 gas through the solution and incubated at 37°C for 1 hour. The solution was made 5 mM in iodoacetic acid and incubated at 37°C in the dark for a further 2 1/2 hours. The solution was then made 15 mM in β-mercaptoethanol and chromatographed on a column of Sephadex G-25 superfine equilibrated in 9% formic acid. The void fraction was pooled and lyophilized. The individual subunits were resolved by

chromatography on a 1.0 x 30 cm column of Superose 12 equilibrated with 9% formic acid.

Example 3B

Amino terminal sequencing of individual subunits

Bovine GlcNAc-phosphotransferase, 0.5 mg was equilibrated with sodium dodecyl sulfate, electrophoresed on a 6% polyacrylamide gel in the presence of sodium dodecyl sulfate. The resolved subunits were then electro-transferred to a PVDF membrane and the protein bands detected by staining with Coomassie Blue. The bands corresponding to the individual subunits were then excised with a razor blade and subjected to amino-terminal sequencing in an Applied Biosystems Model 492 protein sequencer. The amino terminal sequence of the α-subunit was Met Leu Leu Lys Leu Leu Gln Arg Gln Arg Gln Thr Tyr (SEQ ID NO:26). The amino terminal sequence of the β Subunit is Asp Thr Phe Ala Asp Ser Leu Arg Tyr Val Asn Lys Ile Leu Asn Ser Lys Phe Gly Phe Thr Ser Arg Lys Val Pro Ala His (SEQ ID NO:27). The amino terminal sequence of the γ-subunit is Ala Lys Met Lys Val Val Glu Glu Pro Asn Thr Phe Gly Leu Asn Asn Pro Phe Leu Pro Gln (SEQ ID NO:28).

Example 3C

Internal amino acid sequence of the β- and γ-subunits

The resolved β- and γ-subunits from example 3B were treated with trypsin at a 1/40 mass ratio overnight at 37°C in 0.1 M Tris-HCl, pH 8.0. The tryptic fragments were then resolved by reverse phase chromatography on a C18 column equilibrated with 0.1% trifluoroacetic acid and developed with a linear gradient in acetonitrile. Well resolved peaks were then subjected to amino terminal sequencing as described in example 3B. The peptides sequenced from the β-subunit had the sequences Ile Leu Asn Ser Lys (SEQ ID NO:29), Thr Ser Phe His Lys (SEQ ID NO:30), Phe Gly Phe The Ser Arg (SEQ ID NO:31), and Ser Leu Val Thr Asn Cys Lys Pro Val Thr Asp Lys (SEQ ID NO:32). The peptide

sequenced from the γ-subunit had the sequence Leu Ala His Val Ser Glu Pro Ser Thr Cys Val Tyr (SEQ ID NO:33). A second peptide sequence from the γ-subunit was obtained by chymotryptic digestion with the sequence Asn Asn Pro Phe Leu Pro Gln Thr Ser Arg Leu Gln Pro (SEQ ID NO:34).

Example 3D

Internal amino acid sequence of the α-subunit

Internal peptide sequences of the α-subunit were obtained as follows. Bovine GlcNAc phosphotransferase was reduced, alkylated, electrophoresed and transferred to PVDF as previously described. The α-subunit band was excised and tryptic peptides generated by in situ digestion with trypsin, eluted with acetonitrile/trifluoroacetic acid and fractionated by reverse phase HPLC. Individual peaks were then examined by Matrix Associated Laser Desorption-Ionization-Mass Spectroscopy (MALDI-MS) and peaks containing a single mass were subjected to amino terminal sequencing as above. The peptide sequences determined from the α-subunit are Val Pro Met Leu Val Leu Asp Xaa Ala Xaa Pro Thr Xaa Val Xaa Leu Lys (SEQ ID NO:35) and Glu Leu Pro Ser Leu Tyr Pro Ser Phe Leu Ser Ala Ser Asp Val Phe Asn Val Ala Lys Pro Lys (SEQ ID NO:36).

Example 4

Cloning the human GlcNAc-phosphotransferase α/β-subunit cDNA

The amino-terminal protein sequence determined from the isolated bovine β-subunit was used to search the Expressed Sequence Tag (EST) data base using the program tblastn. Altschul, S. F., Gish W., *et al.* (1990). "Basic Local Alignment Search Tool." *Journal of Molecular Biology* 215: 403-410. This search identified a partial mouse cDNA previously identified during a positional cloning strategy. Cordes, S. P. and Barsh, G. S. (1994). "The mouse segmentation gene *kr* encodes a novel basic domain-leucine zipper transcription

factor." *Cell 79:* 1025 - 11034.

A forward PCR primer was designed based on the mouse sequence and used with an oligo dT reverse primer for RT-PCR amplification of a 1,848 bp product using mouse liver poly A RNA as template. The PCR product was cloned and sequenced and proved to contain all the determined β-subunit sequences, demonstrating it encoded the murine β-subunit.

The human β-subunit cDNA was cloned by screening a size selected human placental cDNA library (Fischman, K., Edman J. C., *et al.* (1990). "A murine *fer* testis-specific transcript (*fer*T encodes a truncated fer protein." *Molecular and Cellular Biology* 10: 146 - 153) obtained from ATCC with the random hexamer labeled murine β-subunit cDNA under conditions of reduced stringency (55°C, 2XSSC). The remaining portion of the α/β-subunit precursor cDNA was cloned by a combination of a walking strategy beginning with the portion of the cDNA encoding the human β-subunit and standard library screening strategies. Additionally, EST data base searches were used to identify clones containing portions of the human α/β cDNA, which were obtained from the corresponding repositories and sequenced. Together these strategies allowed the determination of the full length human α/β-subunits precursor cDNA sequence. A clone containing this sequence was assembled using the appropriate fragments and cloned into pUC19. The 5597 bp sequence is given in Sequence NO:4 and contains DNA sequences predicted to encode protein sequences homologous to all of the amino terminal and internal peptide sequences determined from the bovine α- and β-subunits.

Example 5

Cloning the human GlcNAc-phosphotransferase γ-subunit cDNA

The γ-subunit amino terminal and tryptic peptide sequences were used to search the Expressed Sequence Tag (EST) data base using the program tblastn. Altschul, S. F., Gish W.,

et al. (1990). "Basic Local Alignment Search Tool." *Journal of Molecular Biology* 215: 403-10. Three human EST sequences were identified which were highly homologous to the determined bovine protein sequences. cDNA clone 48250 from which EST sequence 280314 was determined was obtained from Genome Systems and sequenced using standard techniques. This clone contained a 1191 bp insert which contained all the determined protein sequences and appeared to contain a signal sequence 5' of the determined amino terminal sequence. The clone however lacked an initiator methionine or any 5' non-coding sequence. The 5' portion of the cDNA was obtained by PCR. the reverse primer 5'-GCGAAGATGAAGGTGGTGGAGGACC-3' (SEQ ID NO:37) and a T7 promoter primer were used in a reaction along with template DNA from a human brain cDNA library in pCMV-SPORT(GIBCO). A 654 bp product was obtained, cloned in pCR2.1 and sequenced. The sequence demonstrated the amplified product contained 23 bp of 5' non-coding sequence, the initiator methionine and the signal peptide identified in EST 280314. A full length cDNA for the γ-subunit (pBC36) was assembled by ligating a 75 bp EcoRI-ApaI fragment from the cloned PCR product, an ApaI-NotI fragment from clone 48250 and EcoRI-NotI cut pcDNA3 (Invitrogen).

Example 6

Cloning the human GlcNAc-phosphotransferase α/β-subunit gene

Plasmid DNA was prepared from a human brain cDNA library (Life Technologies) according to the manufacturers protocol. This DNA was used as template for PCR using primers with the sequences 5'-TGCAGAGACAGACCTATACCTGCC-3' (SEQ ID NO:38) and 5' ACTCACCTCTCCGAACTG-GAAAG-3' (SEQ ID NO:39) using Taq DNA polymerase and buffer A from Fischer Scientific using 35 cycles of 94°C 1 minute, 55°C 1 minute, and 79°C 1 minute. A 106 bp product was obtained, purified by agarose gel

electrophoresis, isolated by GeneClean (Biol01) and cloned into pCR2. DNA sequencing determined the resulting plasmid pAD39 contained a 106 bp insert which was excised by digestion with EcoRI and submitted to Genome Systems for screening of a human genomic BAC library. Four human BACs were identified and BAC #14951 was sequenced. For sequencing BAC #14951 was submitted to a colleague's laboratory at the University of Oklahoma. The BAC was then fragmented by nebulization, and fragments cloned into pUC18 and shotgun sequenced. Contigs were generated by computer analysis and gaps closed by primer walking strategies. The sequence of the BAC spans 177,364 bp. The GlcNAc-phosphotransferase α/β-subunits precursor gene spans ~80 kb and is arranged as 21 exons.

Example 7

Cloning the human GlcNAc-phosphotransferase γ-subunit gene

The human γ-subunit gene was identified by blastn searching of the NCBI High Throughput Genomic Sequence (HGTS) database with the full length human Subunit cDNA sequence. The search identified a clone HS316G12(gi 4495019) derived from human chromosome 16 which contained the human γ-subunit gene. The human GlcNAc-phosphotransferase γ-subunit gene spans about 12 kb and is arranged as 11 exons. Exons 1-3 and 4-11 are separated by a large intron of about 9 kb.

Example 8

Preparation of modified expression plasmid for the human GlcNAc-phosphotransferase α/β-subunits precursor cDNA

An expression vector for the GlcNAc-phosphotransferase α/β cDNA was constructed in pcDNA3.1(+) as follows. Two upstream ATG's in the 5'-noncoding sequence of the human GlcNAc-phosphotransferase cDNA were removed and the Kozak sequence were

modified as follows. Two fragments from pAD98, which was the human GlcNAc-phosphotransferase ct/p cDNA cloned into pcDNA3.1(+), were excised. A 1068 bp XhoI-PstI fragment and a 9746 bp NheI-XhoI fragment were ligated with oligonucleotides with sequences 5'-CTAGCCACCATGGGGTTCAAGCTCTTGCA-3' (SEQ ID NO:40) and 5'-AGAGCTTGAACCCCATGGTGG-3' (SEQ ID NO:41) generating pAD105. The poly A sequence near the 3' end of the cDNA clone was removed by ligating a NheI-BglII fragment from the cDNA with NheI-BamHI cut vector pcDNA3.1(+) generating pAD128.

Example 9

Preparation of an expression plasmids for the human GlcNAc-phosphotransferase α/β subunits precursor cDNA

DNA sequencing of pAD128 identified deletion of an A in an AAAAA sequence (positions 2761-2765 shown in SEQ ID NO:4) that disrupted the coding sequence. Plasmid pAD130 was constructed in an attempt to correct this by ligating a 5929 bp NheI-MfeI fragment and a 2736 bp NheI-AgeI fragment (both from pAD128 with a 515 bp MfeI-AgeI fragment derived from pAD124). Plasmid pAD130 was then grown and subsequent sequencing of plasmid pAD130 demonstrated that the AAAAA sequence had reverted to AAAA again indicating instability in the sequence at this point.

In order to eliminate this instability the first AAA (position 2761-2763 shown in SEQ ID NO:4) that codes for lysine was changed to AAG (also coding for lysine) so that the unstable AAAAA sequence was changed to a stable AAGAA without altering the encoded amino acid. Plasmid pAD130 was corrected by removing a 214 bp MfeI-DraIII fragment and replacing it with a fragment with the correct sequence. The correct MfeI- DraIII fragment was prepared by PCR using pAD130 as a template with forward primer 5'-GAAGACACAATTGGCATACTTCACTGATAGCAAGAATACTGGGAGGC

AACTAAAAGATAC-3' (SEQ ID NO:42) (oligo TTI 25 with desired AAGAA sequence as underlined) and reverse primer 5'-ACTGCATATCCTCAGAATGG-3' (SEQ ID NO:43) (oligo TTI 24). The PCR fragment was subcloned into the EcoRV site of pBluescript KS II(+) (Stratagene) generating pMK16. The insert was sequenced for confirmation and the 215 bp MfeI- DraIII fragment was prepared. To avoid MfeI- DraIII sites on the vector pcDNA 3.1(+) (Invitrogen), the NheI-XbaI fragment was prepared from pAD130 and subcloned into the XbaI site of pUC19 (Life Technologies) to construct pMK15. pMK15 was cleaved with MfeI and DraIII and the 6317 bp fragment was purified and ligated with the MfeI- DraIII fragment from pMK16 to form pMK19 containing the desired stable sequence in pUC19.

The corrected cDNA for the α/β subunit was excised from pMK19 as a KpnI-XbaI fragment and subcloned between the KpnI and XbaI sites of pcDNA6/V5/His-A and designated pMK25. Plasmid pMK25 containing the cDNA as shown in SEQ ID NO:20 where the nucleotide sequence for the modified human α/β-subunit precursor cDNA is shown in nucleotides 1-3768. This sequence corresponds to and is a modification of the nucleotide sequence 165-3932 shown in SEQ ID NO:4.

Example 10

Construction of Expression vectors for soluble, human GlcNAc-phosphotransferase α/β subunits precursor cDNA

Plasmid pMK19 was digested with BglII (cutting at positions 255 and 2703 shown in SEQ ID NO:20) and self-ligated to reduce the length of the cDNA to be amplified from approx. 3.5 kb to 1 kb so that the 5' and 3' ends of the cDNA can be modified by PCR to remove the transmembrane domains of the α and β subunits of human GlcNAc-phosphotransferase and used to construct expression vectors to produce soluble

GlcNAc-phosphotransferase. This plasmid was designated pMK21. The strategy is that the nucleotides encoding the first 44 amino acids containing the transmembrane domain of the α subunit (nucleotides 1-132 of SEQ ID NO:20) are replaced with a HindIII site, and nucleotides encoding the last 47 amino acids containing the transmembrane domain of the β subunit (nucleotides 3628-3768 of SEQ ID NO:21) are replaced with a stop codon and a XbaI site.

Plasmid pMK21 was used as a template for PCR with the following primers: A forward primer (5'-TGGTTCTGAAGCTT*AGCCGAGATCAATACCATG*-3' (SEQ ID NO:44), oligo TTI 76) containing a HindIII site (underlined) and a sequence complementary to nucleotides 133 to 151 of SEQ ID NO:20 (italics), which will produce the 5'-end of a PCR fragment that removes the coding sequence of the first 44 amino acids comprising the putative transmembrane domain of the α subunit. A reverse primer (5'-TAGTACACTCTAGActacta*CTTCAATTTGTCTCGATAAG*-3' (SEQ ID NO:45), oligo TTI 78) containing a XbaI site (underlined), two stop codons (lower case) and a sequence complementary to nucleotides 3608 to 3627 of SEQ ID NO:21 (italics), which will produce the 3'-end of a PCR fragment that removes the coding sequence of the last 47 amino acids comprising the putative transmembrane domain of the β subunit and replaces it with two stop codons. The resulting PCR fragment was subcloned into the EcoRV site of pBluescript KS II+ (Stratagene). This plasmid, designated pMK42, was sequenced to ensure no errors were introduced by PCR. The BglII- BglII fragment (positions 255-2703 shown in SEG ID NO:20) which was previously removed was subcloned back into the BglII site of pMK42. The orientation of this fragment was determined to be correct and this plasmid was designated pMK49. Thus, plasmid pMK49 contained a cDNA comprising a 5' HindIII site and a 3' XbaI site flanking a coding region for the human GlcNAc-phosphotransferase α/β

subunits precursor cDNA with the α subunit putative transmembrane domain deleted and the putative transmembrane domain of the β subunit replaced with two stop codons (soluble α/β-cDNA).

This "soluble α/β-cDNA" can now be conveniently sub-cloned into vectors constructed to contain the HPC4 epitope (used for rapid purification of the soluble enzyme) and different secretion signal peptides. These pcDNA6/V5/His-A+tag) vectors were constructed as follows:

Synthetic oligonucleotide cassettes containing a 5'-NheI site and a 3'-HindIII site flanking nucleotide sequences coding for different secretion signal peptides and the nucleotide sequence coding for the HPC4 epitope were inserted into plasmid pcDNA6/V5/His-A cut with NheI and HindIII. The following plasmids were prepared with the indicated cassette:

1. pMK45 - mouse immunoglobulin Kappa chain signal peptide (sequence in italics) and HPC4 epitope (sequence underlined)

CTAGCCGCCACC *ATGGAGACAGACACACTC CTGCTATGGGTACTGCTGCTC*
GGCGGTGGTACC TC TGTCT GTGTGAGGACGATACCCATGACGACGAG
TGGGTTCC AGGT TC CACTGGTGA CGAAGATCAGGTAGATCCGCGGTT AATC
ACCCAAGGTCCAAGGTGACCACTGCTTC TAGTCCAT CTAGGCGCCAATTAG
GACGGTA
CT GCCATTCGA (SEQ ID NO:46)

1. pMK44 - a transferrin signal peptide sequence (in italics) and HPC4 epitope (sequence underlined)

CTAGCGGTACCAT*GAGATT AGCAGTAGGCGCC TT ATTAG TATGCGC AGTACT C*

CGCCATGGTACTCTAATCGTCATCCGCGGAATAATCATACGCGTCATGAG

GGATTAT GTC TCGCAG AAGATCAGGTAGATCCGC GGTT AATCGACGGTA

CCTTATACAGAGCGTCTTCTAG TCCAT CTAGGCGCCAAT TAGCTGCCATTCGA

(SEQ ID NO:47)

1. pMK43 - a transferrin secretion peptide sequence modified to satisfy a Kozak's sequence(sequence in italics) and HPC4 epitope (sequence underlined),

CTAGCCGCCACCATGGGATT *AGCAGTAGGCGCCTT ATT AGT ATGCGC AGT*

CGCCGGTGGTACCCTAATCGTCATCCGCGGAATAATCATACGCGTCA

ACT CGGATTAT GT C TCGCA GAAGATCAGGTAGATCCGC GGTTAATCGACG

TGAGCCTAATACAGAGCGTCTT CTAGT CCATCTAGGCGCCAAT TAGCTGC

GTA

CATTCGA (SEQ ID NO:48)

The cDNA encoding "soluble α/β subunits" can be obtained as a HindIII- XbaI fragment from pMK49 and inserted into the plasmid pMK43 to form pMK50; pMK44 to form pMK51, and into pMK45 to form pMK52, plasmids capable of encoding the α/β subunits of human GlcNAc-phosphotransferase with putative transmembrane domains

deleted, with different signal peptides and all having the HPC4 epitope tag to facilitate purification of the soluble, secreted enzyme.

Example 11

Construction of Expression vectors for the human GlcNAc-phosphotransferase γ subunit precursor cDNA

The human GlcNAc-phosphotransferase γ-subunit precursor cDNA was obtained from plasmid pAD133 in pAC5.1/V5-His by cutting with EcoRI. This cDNA was inserted into EcoRI digested pcDNA6/V5/His-A to form plasmid pMK17 containing cDNA as shown in SEQ ID NO:5. Plasmid pMK17 was digested with MluI (position 124-129 as shown in SEQ ID NO:5) and EcoRI (position 1103-1108 as shown in SEQ ID NO:5) and the 980 bp MluI- EcoRI fragment was then subcloned in pBluescriptKSII(+) with a synthetic double stranded cassette having an HindIII site and a MluI site flanking a nucleotide sequence including positions corresponding to 95-123 as shown in SEQ ID NO:5 thereby removing the nucleotide sequence encoding the amino terminal, 24-amino acid signal peptide in plasmid pMK26. Plasmid pMK26 was sequenced to ensure its sequence. The correct cDNA from pMK26, which encodes amino acids for the human GlcNAc-phosphotransferase γ subunit with the signal peptide removed, is then excised from pMK26 by HindIII and EcoRI digestion and placed into plasminds pMK43 to form pMK58; pMK44 to form pMK59, and into pMK45 to form pMK64, plasmids capable of encoding the γ subunit of human GlcNAc-phosphotransferase with its signal peptide deleted, with different signal peptides and all having the HPC4 epitope tag to facilitate purification of the soluble, γ subunit.

To evaluate the behavior of α/β/γ secreted products, the α/β subunit precursor and the γ subunit were co-expressed in the bi-cistronic vector pIRES (Clontech). This was accomplished by subcloning α/β and γ cDNAs expressing the desired subunit with a selected

signal peptide and the HPC4 Tag into NheI site (MCS-A) and XbaI site (MCS-B) of pIRES, respectively.

Example 12

Transient expression of the α/β and γ subunits of human GlcNAc-phosphotransferase in 293T Cells

Plasmids were transfected into 293T cells using Fugene6 (Roche) according to manufacturer's instructions. Culture media was collected 23 h, 44.5 h and 70 h after transfection. Aliquots of media containing expressed protein was captured on anti-HPC4 monoclonal antibody (U.S. Patent No. 5,202,253) conjugated with Ultralink beads (Pierce) by overnight incubation at 4 °C. The beads were washed to remove unbound protein and assayed directly for phosphotransferase activity as described previously (REF).

Plasmids used for expression all containing a sequence encoding for the HPC4 tag were as follows:

1. pMK50 -modified transferrin secretion peptide and α/β subunit in pcDNA6/V5/His-4
2. pMK51 -transferrin secretion peptide and α/β subunit in pcDNA6/V5/His-4
3. pMK52 - mouse immunoglobulin secretion peptide and α/β subunit in pcDNA6/V5/His-4
4. pMK75 - modified transferrin secretion peptide and α/β subunit and modified transferrin secretion peptide and γ subunit in pIRES
5. pMK81 -transferrin secretion peptide and α/β subunit and transferrin secretion peptide and γ subunit in pIRES
6. pMK76 - mouse immunoglobulin secretion peptide and α/β subunit and mouse immunoglobulin secretion peptide and γ in pIRES

The relative amounts of expression detected by assay for phosphotransferase using methyl-α-D-mannoside and UDP-[β-^{32}P]-GlcNAc as substrates with cell transfected with pcDNA6/V5/His-4 as controls is shown in Figure 4.

Example 13

Expression and purification GlcNAc-phosphotransferase α/β/γ

For expression and purification of the enzyme, a modified expression plasmid is constructed in a modified expression vector derived from pEE14. The plasmid directs the synthesis of a soluble epitope tagged GlcNAc-phosphotransferase molecule. The α/β-subunit precursor is modified as follows: The 5' portion of the cDNA which encodes the α-subunit cytoplasmic and transmembrane domain is deleted and replaced with nucleotides which encode the transferrin signal peptide followed by amino acids which encode the epitope for monoclonal antibody HPC4. The 3' portion of the cDNA is modified by the insertion of a stop codon before the β-subunit transmembrane segment. The vector pEE14.1 (Lonza Biologics) is modified by the insertion of a 850 bp MluI-NcoI fragment containing a modified vascular endothelial growth factor (VEGF) promoter at the unique MluI site in pEE14.1. This vector encoding the modified GlcNAc-phosphotransferase α/β-subunit precursor is co-transfected with a wild type γ-subunit construct containing the VEGF promoter in pEE14.1 into CHO-K1 cells using Fugene6 and plated into 96 well plates. Transfectants are selected in 25 μm methionine sulfoximine and the plasmid amplified by selection in 96 well plates with 50 μM, 100μM, 250μM, and 500 μM methionine sulfoximine. Clones are picked into duplicate 96 well plate and the highest expressing clones selected by dot blotting media and immuno-detection with monoclonal antibody HPC4. The highest expressing clone is expanded into cell factories. The recombinant soluble epitope tagged GlcNAc-phosphotransferase is purified from the media by

chromatography on monoclonal antibody HPC4 coupled to Ultralink in the presence of 5 mM $MgCl_2$ and 1 mM $CaCl_2$. The soluble epitope tagged GlcNAc-phosphotransferase is eluted with 5 mM EGTA and 5 mM $MgC1_2$.

Example 14

Preparation of monoclonal antibodies specific for bovine phosphodiester α-GlcNAcase

Murine monoclonal antibodies specific for bovine phosphodiester α-GlcNAcase were generated by immunization of mice with a partially purified preparation of phosphodiester α-GlcNAcase. Spleens were then removed from immune mice and fused with SP2/O myeloma cells according to standard techniques (Harrow, E. and Lane, D. (1988). *Antibodies: a laboratory manual,* Cold Spring Harbor Laboratory). Hybridomas were plated in eight 96-well plates and grown until hybridomas were visible. Hybridomas secreting antibodies to phosphodiester α-GlcNAcase were identified measuring phosphodiester α-GlcNAcase activity in immunoprecipitates prepared by incubation of a partially purified preparation of phosphodiester α-GlcNAcase with pooled hybridoma supernatants. Pools from 16 and 4 wells were assayed followed by individual wells. Monoclonal UC1 was identified by this protocol and coupled to Ultralink™ for use in purification of phosphodiester α-GlcNAcase.

Example 15

Purification of bovine phosphodiester α-GlcNAcase

Bovine calf liver (1 kg) was homogenized in 0.05 M Imidazole-HCI, pH 7.0, 0.15 M NaCI, 0.01 M EDTA and a washed post-nuclear supernatant was prepared. Membranes were collected by centafugation at 30,000 x g for 30 minutes and washed three times with the above buffer. Membrane proteins were then solubilized in buffer containing 2% Triton X-100, 0.05% deoxycholate and insoluble material removed by centrifugation, as before. The solubilized membrane fraction was incubated with 20 ml of monoclonal antibody UCl

coupled to Ultralink™ (substitution 5 mg/ml) with constant rotation for 16 hours at 4°C. The UC1-Ultralink™ was collected by low speed centrifugation. packed into a column and washed with 0.025 M Tris-HCI, pH 7.4, 0.3% Lubrol, followed by two column volumes of 0.5 M NaHCO3, pH 8.0, 0.3% Lubrol. Phosphodiester α-GlcNAcase was then eluted with 0.5 M NaHCO3, pH 10.0, 0.3% Lubrol and collected in 1/10 volume of 1.0 M Tris-HCI, pH 5.5.

Example 16

Amino acid sequencing of bovine phosphodiester α-GlcNAcase

Example 16A

Amino-terminal sequence of bovine phosphodiester α-GlcNAcase

Bovine phosphodiester α-GlcNAcase was bound to a 0.25 ml column of POROS HQ and step-eluted with buffer containing 0.5 M NaCl. Fractions containing phosphodiester α-GlcNAcase activity were identified by phosphodiester α-GlcNAcase assay, pooled and absorbed to a ProSorb Sample Preparation Cartridge (Perkin Elmer) and subjected to amino acid sequencing in an Applied Biosystems Model 492 Protein Sequencer operated according to the manufacturer's instructions. The sequence Asp-Xaa-Thr-Arg-Val-His-Ala-Gly-Arg-Leu-Glu-His-Glu-Ser-Trp-Pro-Pro-Ala-Ala-Gln-Thr-Ala-Gly-Ala-His-Arg-Pro-Ser-Val-Arg-Thr-Phe-Val was obtained.

Example 16B

Internal sequence of bovine phosphodiester α-GlcNAcase

Bovine liver phosphodiester α-GlcNAcase was concentrated to 10 µl in a Speed Vac, combined with 30 µl 0.1 M Tris-HCI, pH 7.4, 8 M guanidine-HCI, and 2-4 µl 25 mM DTT and incubated at 50°C for I hour. Iodoacetamide 2.4 µl 50 µM was then added and the incubation was continued for I hour. The reaction mixture was then desalted on a column of

Sephadex G25 superfine as described for GlcNAc-phosphotransferase and digested with trypsin. The peptides were fractionated by HPLC and sequenced as described for GlcNAc-phosphotransferase. The sequences determined are Arg Asp Gly Thr Leu Val Thr Gly Tyr Leu Ser Glu Glu Glu Val Leu Asp Thr Glu Asn and Gly Ile Asn Leu Trp Glu Met Ala Glu Phe Leu Leu Lys.

Example 17

Cloning the human phosphodiester α-GlcNAcase cDNA

The phosphodiester α-GlcNAcase tryptic peptide sequences were used to search the EST data bases as described for GlcNAc-phosphotransferase above. Three EST sequences were identified which contained the human phosphodiester α-GlcNAcase cDNA and clone ATCC #367524 was obtained and a ~700 bp EcoRI-NotI fragment was excised from this clone and used to probe a human liver cDNA library in the vector TriplEx. Several clones were identified and sequenced, one of which (clone 6.5) proved to contain a nearly full length cDNA for the human phosphodiester α-GlcNAcase. The genomic clone described in Example 18 demonstrated that clone 6.5 was missing only the initiator methionine.

Example 18

Cloning the human phosphodiester α-GlcNAcase gene

The human phosphodiester α-GlcNAcase gene was identified by searching the NCBI database nr with the human phosphodiester α-GlcNAcase cDNA using the program blastn. The genomic sequence was determined during the sequencing of a clone from chromosome 16p13.3 and deposited 06-Mar-1999 in GenBank as an unidentified sequence of 161264 bp with the accession number AC007011. The gene spans about 12 kb of genomic DNA on chromosome 16.13 and is arranged in 11 exons.

Example 19

Construction of an expression vector for human phosphodiester or α-GlcNAcase

An expression vector for human phosphodiester α-GlcNAcase was prepared as follows: The 5' end of the sequence of clone 6.5 was modified by PCR amplification of the 5' end of the cDNA with a forward primer with the sequence 5'-GGAATTCCACCATGGCGACCTCCACGGGTCG-3' (SEQ ID NO:49) and a reverse primer 5'-TGACCAGGGTCCCGTCGCG-3' (SEQ ID NO:49). This served to add a consensus Kozak sequence and initiator methionine to the sequence of clone 6.5. The ~500 bp PCR product was purified, digested with EcoRI and BamHI and ligated into pcDNA3.1(-) which was sequenced. This construct was then digested with BamHI and HindIII and ligated with a ~1600 bp BamHI-HindIII fragment containing the 3' portion of the cDNA from clone 6.5 generating the full length expression plasmid.

Example 20

Host cell preparation for human phosphodiester α-GlcNAcase

Cos cells were grown in 60 mm plates in Dulbeccos minimal essential media (DMEM) at 37°C in 5% CO_2 until they reached 50-80% confluence. The plates were then washed with OptiMEM I and the cells transfected with the expression vector described in Example 19 using Lipofectamine Plus (GIBCO BRL Life Technologies) according to the manufacturers instructions. Cells were harvested at 48 hours, a solubilized membrane fraction prepared and assayed for phosphodiester α-GlcNAcase activity.

Example 21

Expression and purification of soluble recombinant human phosphodiester α-GlcNAcase

For expression and purification of the enzyme, a modified expression plasmid is constructed in a modified expression vector derived from pEE14.1. The plasmid directs the

synthesis of a soluble epitope tagged phosphodiester α-GlcNAcase molecule. The phosphodiester α-GlcNAcase precursor is modified as follows: The 3' portion of the cDNA which encodes the phosphodiester α-GlcNAcase transmembrane and cytoplasmic domains is deleted and replaced with nucleotides which encode the epitope for monoclonal antibody HPC4 followed by a stop codon. The vector pEE14.1 (Lonza Biologics) is modified by the insertion of a 850 bp MluI-NcoI fragment containing a modified vascular endothelial growth factor (VEGF) promoter at the unique MluI site in pEE14.1. This vector encoding the epitope tagged soluble phosphodiester α-GlcNAcase precursor is transfected into CHO-K1 cells using Fugene6 and plated into 96 well plates. Transfectants are selected in 25 μm methionine sulfoximine, and the plasmid amplified by selection in 96 well plates with 50 μM, 100 μM, 250 μM, and 500 μM methionine sulfoximine. Clones are picked into duplicate 96 well plate and the highest expressing clones selected by dot blotting media and immuno-detection with monoclonal antibody HPC4. Media from clones demonstrating the highest level of epitope tag expression is assayed for phosphodiester α-GlcNAcase activity. The highest expressing clone is expanded into cell factories. The recombinant soluble epitope tagged phosphodiester α-GlcNAcase is purified from the media by chromatography on monoclonal antibody HPC4 coupled to Ultralink™ in the presence of 5 mM $MgCl_2$ and 1 mM $CaCl_2$. The soluble epitope tagged phosphodiester α-GlcNAcase is eluted with 5 mM EGTA and 5 mM $MgCl_2$.

Example 22

Construction of an Expression Vector for Soluble, Human Phosphodiester α-GlcNAcase

For expression and purification of the enzyme, a modified expression plasmid is constructed in a modified expression vector derived from the pEE14.1 vector (Lonza Biologics). The plasmid directs the synthesis of a soluble epitope tagged phosphodiester

α-GlcNAcase molecule. The phosphodiester α-GlcNAcase precursor is modified as follows: The 3' portion of the cDNA (1342-1548 of SEQ ID NO: 7) which encodes the phosphodiester α-GlcNAcase transmembrane and cytoplasmic domains was deleted and replaced with nucleotide sequence GAGGACCAGGTGGACCCCAGGCTGATCCAC GGCAAGGAT (SEQ ID NO:51) that encodes the epitope for monoclonal antibody HPC4 (EDQVDPRLIDGKD (SEQ ID NO:52)) followed by a stop codon.

This expression vector was constructed by generating two intermediate plasmids and ligating a fragment from each into pEE14.1 vector (Lonza Biologics) to yield the final expression vector. The first intermediate plasmid designated pKB4 was constructed by ligating the 1034 bp FseI«Bsu36I fragment of phosphodiester α-GlcNAcase (lacking the C-terminal transmembrane and cytoplasmic domains) from clone 6.5, and a Bsu36I-XbaI oligonucleotide fragment that contains the HPC4 epitope into a modified pUC19 vector. The second intermediate plasmid designated pKB5, was constructed by ligating a 850 bp MluI-NcoI fragment containing a modified vascular endothelial growth factor (VEGF) promoter from pcDNA4/HisMax (Invitrogen), a 256 bp BseI-FseI fragment encoding the N-terminus of human phosphodiester α-GlcNAcase from clone 6.5, and an oligonucleotide linker into a modified pUC19 vector. The final expression vector designated pKB6 was constructed by ligating the MluI-FseI fragment from pKB5, and the FseI-HindIII fragment from pKB4 into a MluI/HindIII digested pEE14.1 vector. The plasmid pKB6 contains the nucleotide sequence shown in SEQ ID NO:22.

Expression and purification of soluble recombinant human phosphodiester α-GlcNAcase

Approximately 10^8 293T cells were plated in a cell factory using Dulbecco's modified eagle's medium (DMEM) containing 10% fetal bovine serum in a humidified atmosphere at

37°C with 5% CO2. These cells were transfected with approximately 700 g of pKB6 using 2 ml of transfection reagent Fugene-6 (Roche) for the transient expression of soluble human phosphodiester α-GlcNAcase. After three days of culturing the transfected cells, the medium containing soluble, epitope-tagged, human phosphodiester α-GlcNAcase was collected and applied in the presence of 1 mM CaCl2 to a column of monoclonal antibody HPC4 coupled to Ultralink (Pierce). Affinity purified, epitope-tagged, human phosphodiester α-GlcNAcase (approximately 11 mg) was eluted with buffer containing 5 mM EDTA and stored at -20°C in 50 mM Tris, 150 mM NaCl, 2 mM CaCl2, 50% glycerol, pH 7.2. The enzyme had a specific activity of 500,000 units/mg with [^{3}H]GlcNAc-phosphomannose-α-methyl as a substrate (Kornfeld R, et al., JBC 273:23203-23210).

Example 23

CHO cells expressing recombinant human acid α-glucosidase

The human acid α-glucosidase cDNA was obtained from Dr. Frank Martinuk (Martiniuk, F., Mehler, M., Tzall, S., Meredith, G. and Hirschhorn, R. (1990). "Sequence of the cDNA and 5'-flanking region for human acid alpha-glucosidase, detection of an intron in the 5' untranslated leader sequence, definition of 18-bp polymorphisms, and differences with previous cDNA and amino acid sequences." *DNA Cell Biol* 9(2): 85-94) and cloned into the expression vector pEE14.1. This vector was used to transfect CHO-K1 cells using Fugene6 and plated into 96 well plates. Transfectants were selected in 25 μm methionine sulfoximine, and clones picked and plated into 96 well plates. The plasmid was amplified by selection with 50 μM, 100 μM, 250μM, and 500 μM methionine sulfoximine. Clones were picked into duplicate 96 well plates and the highest expressing clones selected by assay of

the media for acid α-glucosidase activity and the cells for DNA content. The highest expressing clone (Clone 3.49.13) based on acid α-glucosidase activity to DNA content ratio was then expanded into a cell factory. This clone was incubated at 37°C in 5% CO_2 and maintained in Glasgow Minimal Essential Media containing 20 mM TES, pH 7.2, 5% fetal bovine serum.

Example 24

Growth of CHO cells expressing recombinant human acid α-glucosidase in the presence of α-1,2 mannosidase inhibitors

CHO cells expressing human acid α-glucosidase were cultured in Glasgow Modified Minimal Essential Media containing 5% Fetal Bovine Serum, 25 μM methionine sulfoximine, 20 mM TES, pH 7,2, and 7.5 mM l-deoxymannojirimycin-HCl. Alternatively, the cells can be cultured in the above media containing 100 μg/mL l-deoxymannojirimycin-HCl and 25 μg/mL kifunensine.

Example 25

Isolation of recombinant human acid α-glucosidase

Recombinant human acid α-glucosidase was purified from spent tissue culture media as follows: Media was concentrated 10 fold by tangential ultrafiltration with a 30,000 dalton cutoff membrane and dialyzed into 50 mM sodium phosphate, pH 6.5, and applied to a column of ConA Sepharose (Pharmacia). Following a wash with the same buffer to remove the unbound proteins, acid α-glucosidase was eluted with 1.0 M α-methyl glucoside, pooled, concentrated and dialyzed as before. The acid α-glucosidase was then applied to a column of Sephadex G-200 equilibrated with 50 mM sodium phosphate, pH 6.5 and eluted isocratically with the same buffer.

Example 26

Treatment of recombinant human acid α-glucosidase with GlcNAc-phosphotransferase and phosphodiester α-GlcNAcase

Human acid α-glucosidase at 10 mg/ml was incubated in 50 mm Tris-HCl, pH 6.7, 5 mM $MgCl_2$, 5 mM $MnCl_2$, 2 mM UDP-G1cNAc with GlcNAc-phosphotransferase at 100,000 u/mL at 37°C for 2 hours. Phosphodiester α-GlcNAcase, 1000 u/mL was then added and the incubation continued for another 2 hours. The acid α-glucosidase was then repurified by chromatography on Q-Sepharose, and step elution with NaCl.

Example 27

Characterization of the oligosaccharide structures on modified recombinant human acid α-glucosidase

Recombinant acid α-glucosidase treated or untreated with GlcNAc-phosphotransferase and phosphodiester α-GlcNAcase was digested with N-glycanase (New England Biolabs) or endomannosidase H (New England Biolabs) according to the manufacturer's conditions. The released oligosaccharides were then labeled on the reducing terminus with 2-aminobenzamide and fractionated by HPLC with fluorescent detection according to the manufacturer's instructions (Oxford Glycosystems). Peaks were identified by comparison with standards chromatographed on the same system, and confirmed by digestion with linkage specific glycosidases and/or mass determination by MALDI. The results are shown in Table 1.

Table 1

Enzyme Preparation	M6	M7	M8	M9	1P-Gn	2P-Gn	1M6P	Complex
Rh-GAA (Secreted)	0	0	0	0	0	0	1	99
Rh-GAA (dMM/intracellular)	23	31	23	6	0	0	17	0
Rh-GAA (dMM/intracellular) Ptase-treated	6	11	7	2	12	62	0	0

Referring to Table 1, the data (given in mole percent) show that the Lysosomal enzymes prepared using the GlcNAc-phosphotransferase and phosphodiester α-GlcNAcase of the present invention are highly phosphorylated The data shows that the present invention produces lysosomal enzymes having about 5-10 M6P groups per enzyme compared to about 0-2 for untreated enzymes and enzymes known in the art. When compared to naturally occurring or recombinant lysosomal enzymes, the in vitro-modified preparation is very highly phosphorylated. In the most highly phosphorylated lysosomal enzyme known in the art, the α-galactosidase A described by Matsuura, F., Ohta, M., Ioannou, Y. A. and Desnick. R. J. (1998). "Human alpha-galactosidase A: characterization of the N-linked oligosaccharides on the intracellular and secreted glycoforms overexpressed by Chinese hamster ovary cells." *Glycobiology* 8(4): 329-39, 5.2% of the oligosaccharides are bis-phosphorylated. In marked contrast, 62% of the oligosaccharides on the *in vitro*-phosphorylated acid α-glucosidase, preparation described here contains bis-phosphorylated oligosaccharides. This represents about a 12 fold increase. When the *in vitro* phosphorylated preparation of rh-GAA shown in Table 1 is compared with GAA secreted

from CHO cells by methods known in the art, an even greater increase in phosphorylation is evident, about a 62 fold increase.

Thus, the *in vitro*-phosphorylated GAA is 12-62 fold more phosphorylated than any other described preparation of natural or recombinant lysosomal enzyme. This difference has a major influence on the rate and extent of internalization (Reuser, A. J., Kroos, M. A., Ponne, N. J., Wolterman, R. A., Loonen, M. C., Busch, H. F., Visser, W. J. and Bolhuis, P. A. (1984). "Uptake and stability of human and bovine acid alpha-glucosidase in cultured fibroblasts and skeletal muscle cells from glycogenosis type II patients." *Experimental Cell Research* 155: 178-189).

Example 28

Comparison of cell uptake of recombinant human acid α-glucosidase with or without modification by GlcNAc-phosphotransferase and phosphodiester α-GlcNAcase

Human Pompe disease fibroblasts are obtained from ATCC and cultured in DMEM with 10% fetal bovine serum in 6 well plates and incubated at 37°C in 5% CO_2. Recombinant human acid α-glucosidase with different carbohydrate structures are compared for the rate and extent of internalization. Controls include each preparation incubated with 5 mM mannose 6-phosphate and incubations without added recombinant human acid α-glucosidase. The different preparations to be examined include acid α-glucosidase secreted from CHO cells, acid α-glucosidase secreted from CHO cells in the presence of α1,2-mannosidase inhibitors, acid α-glucosidase secreted from CHO cells in the presence of α1,2-mannosidase inhibitors treated with GlcNAc-phosphotransferase, and acid α-glucosidase secreted from CHO cells in the presence of or1,2-mannosidase inhibitors treated with GlcNAc-phosphotransferase and phosphodiester α-GlcNAcase. Equal amounts of the four different preparations are added to each well and incubated at 37°C for periods varying from

5 minutes to 4 hours. At the end of each incubation period the cell monolayers are washed with phosphate buffered saline containing 5 mM mannose 6-phosphate and the monolayer solubilized in 1% Triton X-100 and assayed for internalized acid α-glucosidase by enzymatic assay.

Applicant and the assignee acknowledge their responsibility to replace these cultures should they die before the end of the term of a patent issued hereon, 5 years after the last request for a culture, or 30 years, whichever is the longer, and their responsibility to notify the depository of the issuance of such a patent, at which time the deposit will be made irrevocably available to the public. Until that time the deposit will be made available to the Commissioner of Patents under the terms of 37 C.F.R. 1.14 and 35 U.S.C. 112.

While the preferred embodiments are shown to illustrate the invention, numerous changes to the materials and methods can be made by those skilled in the art. All such changes are encompassed within the spirit of the invention as defined by the appended claims.

This application claims priority to U.S. Provisional application No. 60/153,831 filed September 14, 1999, and is incorporated herein by reference.